us-09-720-469-2.rag

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Arabidopsis thalia
Arabidopsis thalia
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                             522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
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AAG16462
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1 DFMIQGGDF 9
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mumber of testific predicted by chance to have a	in of equal to the score of the result being printed,	r analysis of the cotal score distribution.	-				Description	(Human cyclophilin	Human ovelonhilia	Himan secreted pro	Human propriate to	maman process	Human cyclopulin	Cyclophilin C, Mu	A. niger peptidyl-	Human cyclophilia		Arabidopsis thalia	
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Claim 4; Page 49; 64pp; Japanese

	Amino acid sequenc Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Yeast PPIase trypt
AAGO5072 AAG16461 AAAG16461 AAAB4878 AAR10764 AAR72918 AAR72918 AAR49292 AAR49292 AAR13320 AAR49292 AAR13319 AAR6953 AAR13319 AAR09983 AAG03983 AAG03983 AAG03983 AAG03983 AAG03983 AAG03983 AAG03983 AAG03983 AAG03983 AAG18026 AAG18036	
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ALIGNMENTS

Tumour antigen peptides derived from cyclophilin B for treatment and diagnosis of tumours $\,\cdot\,$ Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy. Human cyclophilin B peptide fragment #2. AAY69922 standard; peptide; 9 AA. (SUMU) SUMITOMO PHARM CO LTD. (ITOH/) ITOH K. 98JP-0178449. 99WO-JP03360. 11-APR-2000 (first entry) VPI; 2000-116932/10. Itoh K, Gomi S; 409967288-A1. Homo sapiens 24 - JUN-1999; 25-JUN-1998; 29-DEC-1999 AAY69922; RESULT AAY69922 XX S

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of antigenic proteins, peptides, interferon or their encoding DNA, in the manufacture of an agent for the induction of antigen-specific \tau cells -
This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor antigenic peptide; interferon; IFN; antigen-specific T cell; virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell; viral infectious disease; cyclophilin B; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cyclophilin B derived tumor antigenic peptide SEQ ID 17.
                                                                                                                                         100.0%; Score 50; DB 21; Length 9; 100.0%; Pred. No. 4.3e+05;
                                                                                                                                                                            Indels
                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                      AAB46931 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gotoh M, Yamaoka T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SUMU ) SUMITOMO PHARM CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                         WPI; 2001-193144/20
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                                                                                                                                                                                                               1 DFMIQGGDF 9
                                                                                                                                                                                                                                   9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2001
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AAB46931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                              Gaps
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                                                            Indels
           Length
     Score 50; DB 22;
Pred. No. 4.3e+05;
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100.0%; Score 50; L. 100.0%; Pred. No. 4.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein, SEQ ID NO: 4171.
                                                                                                                                                                                                                                                                                                            AAG00090 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-2000 (first entry)
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Best Local Similarity 100.
Matches 9; Conservative
                                                                 9; Conservative
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N-PSDB; AAC00096.
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                                                                                                                                                    (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; S' EST;
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RESULT AABS6701

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Homo sapiens
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                                                                                                    neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antlinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                          Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                              Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                   Human prostate cancer antigen protein sequence SEQ ID NO:1279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 183;
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AAB56701 standard; Protein; 183 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB73302 standard; protein; 211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   disorders such as prostate cancer
                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                99US-0124270
                                             (first entry)
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                            WPI; 2000-587513/55
N-PSDB; AAF15904.
                                                                                                                                                                                                                                                                                                 (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 AA;
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                                                                                                                                                                      Homo sapiens
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the inversion relates to a composition to modulating somatolactogenic function, comprising cyclophilin B (CypB), a mutant of cyclophilin B (CypB) are absent) or an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, e.g., prodactin, growth hormone). The invention also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic function in the animal, and cyclophilin B mutant or a composition on the animal, and cyclophilin B with a somatolactogenic hormone, is useful for treatment of somatolactogenic function in the animal. A composition comprising cyclophilin B with a somatolactogenic function in the animal. A composition comp
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                                                                                                                                                        somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia; c-terminal deletion mutant; mutein.
                                                                                                     cyclophilin B; CypB; prolactin-binding; growth hormone-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR32353 standard; Protein; 212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page -; 21pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-AUG-2000; 2000WO-US21789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rycyzyn MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             · 16-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-211249/21
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 AA;
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WO200113113-A1.
                                                                                                 WO200018934-A1.
                                                                                                                                            10-SEP-1999;
                                                                                                                                                                  30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-2001.
                                                                                                                      06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB73301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                         Peptide
                                                               Protein
                                                                                                                                                                                                                                                                                                       cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB73301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                        A third mammalian cyclophilin, cyp C, was isolated from a cDNA
library prepd. from the murine bone marrow derived stromal cell line
AC 6. This cDNA was isolated from a substracted sub-library contg.
Genes induced by treatment of the stromal cell line with interleukin.

I (IL-1). The message levels for cyp C show a 2-3 fold induction by treatment with IL-1, and this cDNA exhibits a high level of homology with known cyclophilins. Cyp C is distinct from mammalian

Cyclophilins A and B in both sequence and tissue distribution of expression. A fusion protein contg., e.g. amino acids 16-212 of cyp C possesses peptidyl-prolyl isomerase (Pplase) activity which can be completely inhibited by addition of cyclosporin A (CsA). These cyp C intracellular proteins which together form high affinity associations.

For example, the cyp C fusion protein binds to a protein of 77 kD in the absence of GsA, while in the presence fo CsA it no longer binds the child as calcineurin (U.S.S.N.07/740175).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclophilin-like peptidyl prolyl cis-trans isomerase; CYPB; food processing; Endoplasmic retention signal; cis-trans isomerization; protein secretion; toxin; ADP-glucose pyrophosphorylase; glucanase; beta-1,4-endoglucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                            Cyclophilin C; bone marrow; stromal cell line; AC 6; interleukin-1; IL-1; Cyp A; Cyp B; peptidyl-prolyl isomerase; PPIase; cyclosporin A; CsA; ligand; calcineurin.
                                                                                                                                                                                                                                                                     - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 50; DB 14; Length 212; 100.0%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                     Cyclophilin C polypeptide and nucleic acid encoding it for screening a tissue-specific immunosuppressive agent

    A. niger peptidyl-prolyl cis-trans isomerase (CYPB).

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                                                                                                                                                                                                                                                                                                      Claim 9; Page 46 + Fig 1; 63pp; English.
                                                                                                                                                                                          (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY92048 standard; Protein; 212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                             92WO-US06462
                                                                                                                                                                   910S-0740375
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                                                                                                                                                                                                                Weissman IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                          IL-1; cyp A; cyp B;
cyclosporin A; CsA;
                                                                                                                                                                                                                                     WPI; 1993-076431/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 AA;
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                                                                                                                                                                                                                                                 N-PSDB; AAQ36841
         Cyclophilin C.
                                                                                                                                                                                                                Friedman JS,
                                                                                                                                                                   05-AUG-1991;
                                                                            Mus musculus
                                                                                                                                              05-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-2000
                                                                                                 WO9303050-A
                                                                                                                        18-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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IID AAY9
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AC AAY9
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DT 01-A
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CYCI
KW CYCI
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This sequence shows Aspergillus niger cyclophilin-like peptidyl prolyl cis-trans isomerase (CYPB). CYPB is capable of catalyzing the cls-trans isomeration of a peptide bond on the N-terminal side of proline residues in polypeptides. CYPB are useful in methods for increasing the yield of secreted polypeptides from cells. The secreted polypeptides may be enzymes (such as chymosin, thaumatin or alpha-galactosidase) that can be used in food processing, a pest toxin, adenosine diphosphate (ADP)-glucose pyrophosphorylase, a glucanase or beta-1,4-endoglucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptidyl prolyl cis-trans isomerase, designated CYPB, from Aspergillus niger, useful in methods for increasing the yield of secreted polypeptides, such as enzymes used in food processing, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 50; DB 21; Length 212; 100.0%; Pred. No. 0.23;
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                                                                                          1..23
/label= signal_peptide
24..212
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 47-48; 52pp; English.
                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 98GB-002119B
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                                                                                                                                                                                                                                                                                                                                                                                  99WO-IB01669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Derkx PMF, Madrid SM;
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N-PSDB; AAA08772.
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DANI-) DANISCO AS.
Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 AA;
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08-JUN-1
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The invention relates to a composition for modulating somatolactogenic function, comprising cyclophilin B (CypB), a mutant of cyclophilin B (particularly a CypB mutant in which residues 2.12 of the mature protein are absent) or an inhibitor of the interaction of cyclophilin B with a somatolactogenic bormone (e.g., prolactin, growth hormone). The invention also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions using CypB levels in a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic function in the animal, and cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic function in the animal. A composition comprising cyclophilin B is useful in the treatment of short stature, muscale wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition compressent human cyclophilin B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                         Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone .
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                                                                                                                                                                                                Claim 1; Page 17-18; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG16463 standard; Protein; 252 AA.
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99US-0123180
10-AUG-2000; 2000WO-US21789
                            99US-0149752
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                                                                                  Clevenger CV, Rycyzyn MA;
                                                      (UYPE-) UNIV PENNSYLVANIA.
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Matches 9; Conservative
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                                                                                                               WPI; 2001-211249/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 AA;
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                            19-AUG-1999;
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05-MAR-1999;
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990S-0139455.
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99US-0132407.
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99US-0139763
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99US-0139492
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99US-0141842
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99US-0143624
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99US-0144005.
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990S-0147303.
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Pred. No.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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100.0%; Score 50; DB 21; Length 259;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                               Ouery Match
Best Local Similarity 100.0%; Score 50; DB 21; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                       Human cancer associated protein sequence SEQ ID NO:1323.
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                                                                                                                                                                                                        AAB43878 standard; Protein; 291 AA.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the cissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antiallergic; antibacterial; antiviral; cantiniflammatory; antithyroid; antiallergic; antibacterial; antiviral; contropic; vasotropic; antipsoriatic and antianglogenic. The nootropic; vasotropic; antipsoriatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Companies and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentialion or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune collisonalise in the proliferation of the present invention and disorders of haematopoletic cells, autoimmune collisonalise and organ calection, modulate haemostatic or thrombolytic activity, modulate

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Search completed: January 15, 2002, 13:05:27 Job time: 198 sec
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inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibooties, and antegonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The yeast PPIase has the following properties: 1. it isomerises an X-Pro bond in a peptide chain (X = any amino acid); 2. it has single molecular weight about 17,000 (by SDS-PAGE); 3. it has single isoelectric point about 5.2 (by iso-electric focussing) and 4. it is inhibited by cyclosporin A. The enzyme is useful for accelerating protein folding, especially for activating recombinantly produced proteins. The PPIase can be produced in the same cell as the recombinant proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptidyl-prolyl cis-trans isomerase(s) from yeast and E.coli - used to accelerate protein folding
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89JP-0184738.
89JP-0260244.
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                                                                                                    January 15, 2002, 13:00:24; Search time 37.64 Seconds
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GenCore version 4.5
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein – protein search, using sw model
                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                   US-09-720-469-1
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                                                                                                                                                                                                            1 KFHRVIKDF 9
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                                                                                                                                                                           Title:
Perfect score:
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                                                                                                                                                                                                            Sequence:
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                                                                                                    Run on:
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Sequence 34, Appli Sequence 3, Appli Sequence 3, Appli Sequence 8, Appli Sequence 6, Appli Sequence 6, Appli Sequence 5, Appli Sequence 5, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli	Sequence 88, Appl Sequence 98, Appl
US-08-989-045-34 US-08-482-728A-7 US-09-136-442-3 US-08-482-728A-8 US-08-145-995A-6 US-08-145-995A-6 US-08-145-995A-6 US-08-145-995A-6 US-08-148-995A-5 US-08-148-995A-5 US-08-451-747-5 US-08-451-747-5 US-08-451-747-5 US-08-451-747-5 US-08-451-747-5 US-08-451-747-5 US-08-451-747-5 US-08-451-747-13 US-09-134-852-13 US-09-031-219-25 US-09-091-219-25	US-U8-486-099-88 US-08-360-107A-98
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ALIGNMENTS

Sequence 10, Application US/08482728Å
Sequence 10, Application US/08482728Å
GENERALI INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Payan, Donald
APPLICANT: Pour Embarcadero Center, Suite 3400
STREET: Four Embarcadero Center, Suite 3400
STREET: Pour Embarcadero Center, Suite 3400
STREET: California Compatible
COMPUTER READABLE FORM:
APPLICATION NUMBER: US/084482,728A
APPLICATION NUMBER: US/084482,728A
APPLICATION NUMBER: US/084482,728A
APPLICATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 38,304
REFERENC

```
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: NO. 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 49; DB 1; Length 208; 100.0%; Pred. No. 0.036; 1.ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION NUMBER: US 07/740,375
APPLICATION NUMBER: US 07/740,375
APTORNEY, AGENT INFORMATION:
NAME: Dunn, Tracy D. REGISTRATION NUMBER: 34,587
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08142897; Patent No. 5447852; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 1326-2420
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.

Best Local Similarity 100.

Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-142-897-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KFHRVIKDF 9
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                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94105
COUNTRY:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Welssman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
NUMBER OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 0.023;
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                                                                                                                                                                                                                                              Sequence II, Application US/08482728A
Sequence II, Application US/08482728A
Batent No. 5568802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
Annapreser. FISHER WALLEL TO THE TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Flehr, Hobbach, Test, Albritton ADDRESSEE: Flehr, Hobbach, Test, Albritton ADDRESSEE: A Herbert STREET: Four Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California COUNTRY: United States ZIP: 94111-4187 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/482,728A FILING DATE: U7-JUN-1995 CLASSIFICATION: ADDRESSEE: US/08/482,728A FILING DATE: U7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFO WAS A TOORNEY AGENT INFO WAS A STATE OF A STAT
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; Sequence 7, Application US/08142897
; Patent No. 5447852
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Best Local Similarity 100.
Matches 9; Conservative
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MOLECULE TYPE: protein
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35 KFHRVIKDF 43
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35 KFHRVIKDF 43
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Indels

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Pred. No. 0.58; 2; Mismatches

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Best Local Similarity 77.8
Matches 7; Conservative
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32 KFHRLIKNF 40
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Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: 0. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: 6 Herbert
STREET: Four Embarcadero.Center, Suite 3400
CITY: San Francisco
CONTMENTOR: California
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 398-3249
INFORMATION POR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. ...
                                                           NAME: Dunn, Tracy D.
RECISTRATION UNBER: 34 587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CARRACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
APPLICATION NUMBER: US 07/740,375
                      FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                Query Match 89.8
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: un)
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83.7%; Score 41; DB 2; Length 123;

Query Match

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Gaps
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                                                                                                                            APPLICANT: Wisher, Joseph
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton
COUNTRY: United States
ZIP: 941114187
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07-JUN-1995
FILING DATE: 07-JUN-1995
FILING DATE: APARLICATION NUMBER: WASHING WAS
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Patent No. 6150501
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: HONG, XIQIANG
APPLICANT: MA, DONG
TITLE OF INVENTION: NOVEL TYROSINE-CONTAINING
TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REEFERNEC DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEX: (415) 398-3249
TELEX: (415) 398-3249
TELEX: (415) 308-3249
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Pred. No. 2.7;
2; Mismatches
Sequence 19, Application US/08482728A Patent No. 5968802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 83.7%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||:||:|
320 KFHRLIKNF 328
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09028366;
Patent No. 619501
| GENERAL INFORMATION:
| APPLICANT: CARLOW, CLOTILDE K.S.
| APPLICANT: MA, DONG |
| TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS |
| TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS |
| NUMBER OF SEQUENCES: 16 |
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: STREET: 32 TOZE FROAT |
| CITY: Beverly |
| CITY: Beverly |
| CITY: Beverly |
| CITY: Beverly |
| CORRESPONDENCE |
| CITY: Beverly |
| CITY: Beverly |
| CITY: Beverly |
| CITY: Beverly |
| CITY: CARLOW |
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SOCTWARE: FRSESED Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEB-133
                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-
TELECOMMUNICATION INFORMATION:
TELEPRAN: 978-927-5054
TELEPAX: 978-927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: NETELECOMMUNICATION INFORMATION:
TELEPHONE: 978-927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30901
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COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory
REGISTRATION NUMBER: 309
                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: amino acids
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                APPLICATION NUMBER: FILING DATE:
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321 KFHRIIRNF 329
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ZIP: 01915
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US-09-028-366-2
Sequence 2, Application US/09028366
Sequence 2, Application US/09028366
Patent No. 6150501
GENERAL INFORMATION:
APPLICANT: CARLOW CLOTILDE K.S.
APPLICANT: MA, DONG
TITLE OF INVENTION: NOVEL TYROSINE-CONTAINING
TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: New England Blolabs, Inc.
STREET: 32 Tozer Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,366
FILLING DATE:
CLASSIFICATION:
                      ADDRESSEE: New England Biolabs, Inc.
STREET: 32 Tozer Road
CITY: Beverly
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,366
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-133
TELECHONE: 978-927-5054
TELEPHONE: 978-927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 523 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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MOLECULE TYPE: protein

US-09-028-366-4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 7; Conserv
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320 KFHRLIKNF 328
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                                                                                   CITY: Beverly
STATE: MA
COUNTRY: US
ZIP: 01915
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GENERAL INFORMATION:
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US-09-134-852-3
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APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.6%; Score 39; DB 1; Length 176; 87.5%; Pred. No. 2.3;
                                                                                                                                                                                                                     81.6%; Score 40; DB 4; Length 527; 66.7%; Pred. No. 4.2; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-0CT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: RESINICK, DAVID S:
REFRENCE/POCKET UNMBER: 34.235
REGISTRATION NUMBER: 34.235
REGISTRATION NUMBER: 34.235
RELEPROCK/POCKET UNMBER: 34.06
TELEFORMINICATION INFORMATION:
TELEFORMINICATION INFORMATION:
TELEFORMINICATION OF S23-6440
TELEFORMINICATION OF S23-6440
TELEFORMINICATION OF SEQUENCE (617) 523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDMPTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-451-747-3
; Sequence 3, Application US/08451747
; Patent No. 5821107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-145-995A-3
; Sequence 3, Application US/08145995A
Sequence 3, Application US/08145995A
; Setent No. 5480850
; GENERAL INFORMATION:
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 130 WATER STREICITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                Query Match 81.6
Best Local Similarity 66.7
Matches 6; Conservative
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       ; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-028-366-3
                                                                                                                                                                                                                                                                                                                                                                                                                    321 KFHRIIRNE 329
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APPLICANT: CRADM, COUTLDE R.S.
APPLICANT: CRADM, CONTIDE R.S.
APPLICANT: CRADM, CONTIDE R.S.
APPLICANT: CARGOUNG STREET ON THE STREET S
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Patent No. 5482850

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CALCOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: COMPOUNDS
INTERPORT ON: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: 130 WATER STREET
STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                     Ouery Match 79.6%; Score 39; DB 4; Length 269; Best Local Similarity 87.5%; Pred, No. 3.4; Matches 7; Conservative 1; Mismatches 0; Indels
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Pred. No. 7.2;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPOURE: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-CT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34.235
REFRENCE/POCKET NUMBER: 34.06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LELEFAX: (617) 523-640

TELEFAX: (617) 523-6440

TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.6%;
87.5%;
                                                     INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                              single
linear
                 TELEFAX: 978-927-1705
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Best Local Similarity 87.5'
Matches 7; Conservative
                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-028-366-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-145-995A-21
                                                                                                                                                                                                                                                                                                                                                                                 2 FHRVIKDF 9
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66 FHRVIKNF 73
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US-08-145-995A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: HONG, XIQIANG
APPLICANT: HONG, XIQIANG
APPLICANT: HONG, XIQIANG
TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS
TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS
CORRESPONDENCE ADDRESS:
ADDRESSEE: New England Biolabs, Inc.
STREET: 32 Tozer Road
CITY: Beverly
STATE: MA
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB :
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                          FILING LOWIN:
CLIASIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESULT NUMBER: 34.35
REFERENCE/DOCKET NUMBER: 4406
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECAX: (617) 523-3400
TELECAX: (617) 523-6440

FELENAX: 200291 STRE UR
FILING STREAM STREAM SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09028366
Patent No. 6150501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 79.6%; Scr
Best Local Similarity 87.5%; Pri
Matches 7; Conservative 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 978-927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-09-134-852-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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Gaps

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RESULT 15
UG-08-451-747-21
Sequence 21, Application US/08451747
Patent No. 582107
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRECORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC:
STREET: 32 TOZER ROAD
CITY: BEVERLY
STAFE: MASSACHUSETTS
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OMPUTER: IBM PC Compatible
COMPUTER: PATENTIN SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
FILING DATE:
CLACKTENT APPLICATION DATA:
FILING DATE:
CLACKTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILLMS DALE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/145,995

FILLING DATE: 29-0CT-1993

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: WILLIAMS, GREGORY D.

REGISTRATION UNMBER: 30901

REFERENCE/DOCKET NUMBER: NEB-046-DIV

TELECOMMUNICATION INFORMATION:

TELECAMS: (508) 927-5054

TELECAMS: (508) 927-5054

TELERAX: (508) 927-1705

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 591 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: Amino acids

TYPE: Amino acids

TATORNAL TABLESTICS:

TATORNAL TABLESTICS:

TENGTH: 591 amino acids

TATORNAL TABLESTICS:

TATORNAL TAB
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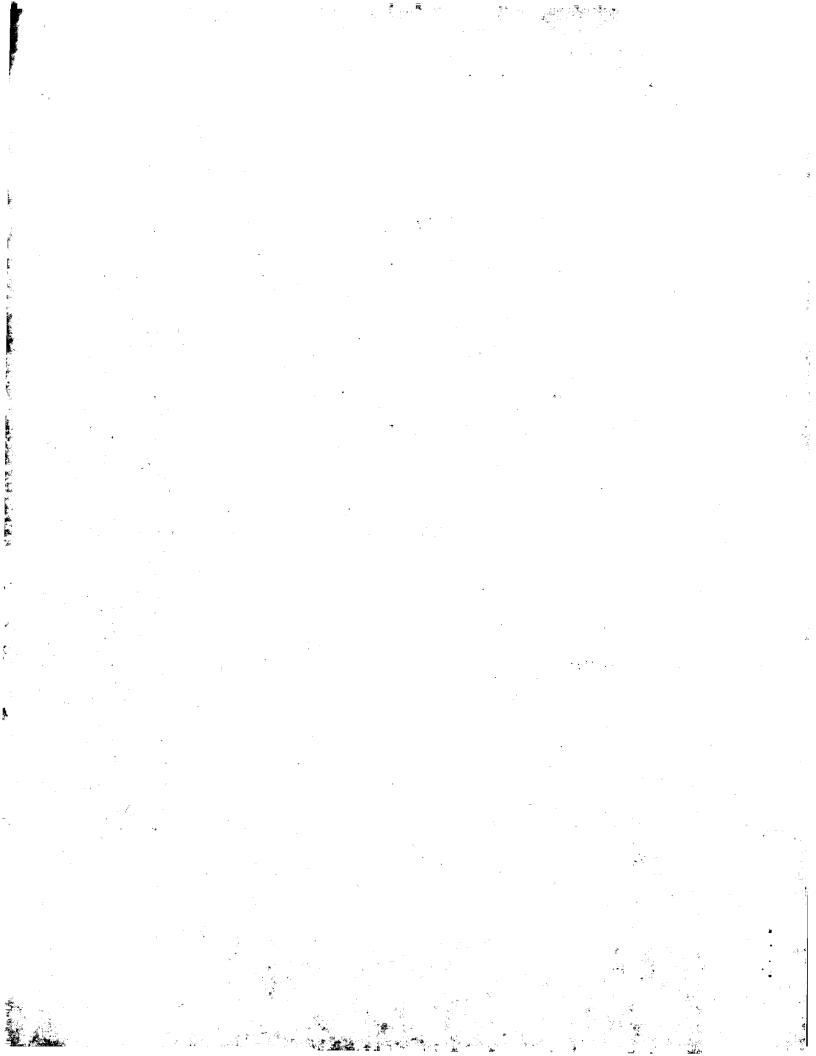
MOLECULE TYPE: protein

US-08-451-747-21
```

ö Gaps ; Query Match 79.6%; Score 39; DB 2; Length 591; Best Local Similarity 87.5%; Pred. No. 7.2; Matches 7; Conservative 1; Mismatches 0; Indels

2 FHRVIKDF 9 ò QQ

Search completed: January 15, 2002, 13:03:58 Job time: 214 sec



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GenCore version 4.5
Copyright (c) 1993 · 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

; Search time 42.04 Seconds (without alignments) 16.308 Million cell updates/sec January 15, 2002, 13:02:29

US-09-720-469-1

1 KFHRVIKDF 9 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		- -				Ü	peptidylprolyl iso			×	peptidyl-prolyl ci	-		Q.	cyclophilin-like p	probable 40 kd pep		>	H	>	_	_							3
SUMMARIES																													
SUMM ID	S71547	A40516	CSHUB	A54204	A56861	F84808	T18578	A40047	A71261	S48567	E86736	T21587	B53422	JC5314	C84777	562327	T23003	T18573	D84533	H69044	T38930	CSBY	828020	S74880	T27371	T27882	T06073	T27034	S57050
DB	- 2	۰ ۵	-	ď	~	ď	~	7	~	ď	~	N	~	-	~	~	N	~	N	~	~	-	C	C	7	~	7	~	7
Length	183	207	208	212	216	199	183	212	215	371	196	204	260	754	164	326	523	201	404	141	155	162	165	171	171	172	172	192	393
% Query Match	100.0	100.0	100.0	100.0	100.0	91.8	89.8	86.8	89.8		•	87.8	7.			83.7			79.6	٠		٠				77.6		٠	
Score	49	49	49	49	49	45	44	44	44	44	43	43	43	43	42	41	41	40	39	38	38	38	38	38	38	38	38	38	38
Result No.		7	m	4	ß	9	7	Φ.	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58

probable cyclophil	natural killer cel	natural killer cel	TMV resistance pro	Ran-binding protei	peptidylprolyl iso	peptidylprolyl iso					peptidylprolyl iso	ò	cyclophylin-like p	hypothetical prote
T41399 T27467	A47328	B47328	T04583	558884	T18577	F81156	T29283	T27373	A53522	JT0686	S30507	T18575	T49181	A84611
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610	1403	1507	1607	3224	147	169	169	173	179	179	182	466	570	1042
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77	77	77	77	7	75	75	75	75	75	75	75	75	75	75
388	38	38	38	38	37	37	37	37	37	37	37	37	37	37
30 31	32	33	34	32	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

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SULT 1	peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat	C.Species: Rattus norvegicus (Norway rat)	C;Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999 C;Accession: S71547	R;Ruecknagel, K.P.; Pfeifer, T.; Rahfeld, J.U.; Schaerfke, M.; Fischer, G.	submitted to the Protein Sequence Database, November 1996	A; Reference number: S71547	A; Accession: S71547	A;Molecule type: protein	A; Residues: 1-183 <rue></rue>	A: Experimental source: liver .	C; Superfamily: peptidylprolyl isomerase; cyclophilin homology	C;Keywords: cis-trans-isomerase	F:11-183/Product: peptidylprolyl isomerase, isoform 20.3K *status experimental <mat></mat>	Fild-1/2/Uomain: cyclophilin homology <cyp></cyp>
RESULT S71547	peptidy N.Alter	C; Speci	C; Date: C; Acces	R; Ruec)	submitt	A;Refer	A; Acces	A; Molec	A; Resic	A; Exper	C; Super	C; Keywo	F; 1-183	T-01:4

Gaps .; 0 Query Match

Query Match

100.0%; Score 49; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels

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A40516
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A40516
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999
C; Accession: A40516
B; Caroni, P.; Rothenfluh, A.; McGlynn, E.; Schneider, C.
J. Biol. Chem. 266, 10739-10742, 1991
A; Treference number: A40516; MUID:91250364
A; Accession: A40516
A; Caroni, P.; Rothenfluh, A.; McGlynn, E.; Schneider, C.
A; Accession: A40516
A; Caroni, P.; Rothenfluh, A.; McGlynn, E.; Schneider, C.
A; Accession: A40516
A; Caroni, P.; Rothenfluh, A.; McGlynn, E.; Schneider, C.
A; Accession: A40516
A; Caroni, P.; Advisorion: A40516
A; Caroni, P.; Advisorion: A40516
A; Caroni, P.; Pid-1999
A; Pid-1999
A; Caroni, P.; Pid-1999
A; Pi

Gaps ó Query Match 100.0%; Score 49; DB 2; Length 207; Best Local Similarity 100.0%; Pred. No. 0.024; Matches 9; Conservative 0; Mismatches 0; Indels

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A Steesation: A56861
A Status: preliminary
A; Molecule type: mRNA
A;
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A; Residues: 9-216 < NOR
A; Residues: 9-216 < NOR
A; Cross-references: EMBL: X58990; NID: 953034; PIDN: CAA41736.1; PID: 953035
C; Comment: This protein is distinguished from peptidylprolyl isomerase A by the prese
C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
C; Superfamily: peptidylprolyl isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell
F;1-33/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptidy)prolyl isomerase (EC 5.2.1.8) CyP-SI precursor - mouse
N;Alternate names: cyclophilin B; cyclophilin-SI; cyclosporin A-binding protein
C;Species: Mus musculus (house mouse)
C;Species: Ms musculus (house mouse)
C;Accession: A56861; B39722; S21835
R;Schumacher, A.; Schroter, H.; Multhaup, G.; Nordhelm, A.
Biochim. Biophys. Acta 1129, 13-22, 1991
A;Title: Murine cyclophilin-SI: a variant peptidyl-prolyl isomerase with a putative s
A;Reference number: A56861; MUID:92096454
                                                                                                                                                                                C;Accession: A54204
R;Schneider, H.; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurini, M.G.; Quesn Biochemistry 33, 8218-8224, 1994
A;Title: Human cyclophilin C: primary structure, tissue distribution, and determinati A;Reference number: A54204; MUID:94304830
peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human
N;Alternate names: cyclophilin C
C;Species: Homo sapiens (man)
C;Date: 22-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A54204
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-212 <SCCH>
A; Cross-references: GB:S71018; NID:9547303; PIDN:AAB31350.1; PID:9547304
A; Experimental source: kidney
A; Note: sequence extracted from NCBI backbone (NCBIN:149387, NCBIP:149388)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB: M60456; NID: 9192864; PIDN: AAA37498.1; PID: 9192865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Map position: 15q21-15q22
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase; cyclosporin A binding
F;37-199/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 49; 100.0%; Pred. No.
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A;Reference number: S21835
A;Accession: S21835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:136196; OMIM:123842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 9-216 <HAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KFHRVIKDF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB: PPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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                                                                                                                                                                                                                                                                                                                            peptidylprolyl isomerase (EC 5.2.1.8) B precursor [validated] - human peptidylprolyl isomerase (EC 5.2.1.8) B precursor [validated] - human N;Alternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin C;Species: Homo sapidans (man) C;Species: Homo sapidans (man) C;Accession: A3918, A39722; A40515; S65742 R;Price, E.R.; Zydowsky, L.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T. Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991 A;Title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl isomer A;Reference number: A39118; MUID:91156714 A;Accession: A39118 A;Molecule type: mRNA A;Accession: A39118 A;Molecule type: mRNA A;Cross-references: GB:M60857; NID:9181334; PIDN:AAA52150.1; PID:9181335 R;Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G. Molecule type: mRNA A;Accession: A3912, MUID:91260697 A;Title: An endoplasmic reticulum-specific cyclophilin. A;Reference number: A39722; MUID:91260697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: protein
A,Residues: 26-30;203 <MAR>
A,Residues: 26-30;203 <MAR>
C,Experimental source: milk
C,Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence C,Comment: This protein binds to and is inhibited by the immunosuppressive drug cyclospe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Molecule type: mRNA, A Molecule type: MR3373; NID:9337998; PIDN:AAA36601.1; PID:9337999
A Moleci the authors' translation begins at an ATG codon in poor context for initiation A Moleci parts of this sequence, including the antho end of the mature form, were confirm R Mariller, C.; Allain, F.; Kouach, M.; Spik, G.
Biochim. Biophys. Acta 1293, 31-38, 1996
A Title: Evidence that human milk isolated cyclophilin B corresponds to a truncated form A Meference number: S65742; MUID:96186273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-208 <4Ms.
A; Cross-references: GB: M60457; NID: 9181249; PIDN: AAA35733.1; PID: 9181250
A; Cross-references: GB: M60457; NID: 9181249; PIDN: AAA35733.1; PID: 9181250
R; Splk, G.; Haendler, B.; Delmas, O.; Mariller, C.; Chamoux, M.; Maes, P.; Tartar, A.;
J. Biol. Chem. 266, 10735-10738, 1991
A; Tille: A novel secreted cyclophilin-like protein (SCYLP).
A; Reference number: A40515; MUID: 91250363
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C; Keywords: cis-trans-isomerase; cyclosporin A binding; glycoprotein; T-cell
E; 12-57 Domain: signal sequence *status predicted <SIG>
E; 203/Product: peptidylprolyl isomerase B #status experimental <MAT>
E; 35-197/Domain: cyclophilin homology <CYP>
E; 140/Binding site: carbohydrate (Asn) (covalent) *status predicted
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C; Function:
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                                                                   1 KFHRVIKDF 9
               6
               1 KFHRVIKDF
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Matches

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Gaps

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peptidylprolyl isomerase (EC 5.2.1.8) (cyclophilin C) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C;Accession: A40047
R;Friedman, J: Weissman, I.
Cell 66, 799-806, 1991
A;Fitler Two cytoplasmic candidates for immunophilin action are revealed by affinity A;Reference number: A40047; MUID:91347379
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A;Reference number: A71250; MUID:98332770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptidylprolyl isomerase (EC 5.2.1.8) TP0947 [similarity] - syphilis spirochete N;Contains: cyclophilin N;Contains: rreponema pallidum subsp. pallidum (syphilis spirochete) C;Dete: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 08-Sep-2000 C;Accession: A71261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RiFraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, rson, J.; Khaladak, H.; Ritchardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
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                                                                                                                                                            Length 183
     A;Introns: 34/3; 87/3; 148/1
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase
F:16-183/Domain: cyclophilin homology <CYP>
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0.24;
                                                                                                                                                     89.8%; Score 44; DB 2;
100.0%; Pred. No. 0.21;
tive 0; Mismatches
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Best Local Similarity 100..
Best Local 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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A; Residues: 1-212 <FRI>
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Best Local Similarity
Matches 8; Conserv
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71 FHRVIKDF 78
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A;Experimental source: clone T01B7
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F;34-216/Product: peptidylprolyl isomerase B #status predicted <MAT> F;43-205/Domain: cyclophilin homology <CYP>
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                                                                                                     Length 216;
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C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
                                                                                                     DB 2;
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Submitted to the EMBL Data Library, October 1995
A:Reference number: Z19867
A:Accession: T24269
A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                100.0%; Score 49; DB 2; 100.0%; Pred. No. 0.025;
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A:Molecule type: mRNA
A:Residues: 1-183 <PAG>
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A;Experimental source: strain Bristol N2
R;Sims, M.
                                                                                                                                                  0; Mismatches
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                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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A; Molecule type: DNA
A; Residues: 1-199 <STO>
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A; Residues: 1-183 <WIL>
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Withternate names: cyclophilin homolog ROC4: protein F21F14.200
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-May-1995 **sequence_revision 19-May-1995 **text_change 19-May-2000
C;Accession: B53422; T47995
R;Lippuner, V.; Chou, I.T.; Scott, S.V.; Ettinger, W.F.; Theg, S.M.; Gasser, C.S. J. Biol. Chem. 269, 7863-7868, 1994
A;Title: Cloning and characterization of chloroplast and cytosolic forms of cyclophil A;Reference number: A53422; MUID:94179146
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A;Residues: 1-260 <LLIP>
A;Cross-references: GB:L14845; NID:g405130; PIDN:AAA20048.1; PID:g405131
A;Cross-references: GB:L14845; NID:g405130; PIDN:AAA20048.1; PID:g405131
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.;
submitted to the Protein Sequence Database, February 2000
                                                                                                                                                                                                               peptidylprolyl isomerase (EC 5.2.1.8) F31C3.1 [similarity] - Caenorhabditis elegans
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                                                                                                                                                                                                                                                   N;Contains: cyclophilin
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Reywords: cis-trans-isomerase F;28-190/Domain: cyclophilin homology <CYP>
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A;Experimental source: cultivar Columbia; BAC clone F21F14
                                                                                                                                                                                                                                                                                                                                           C:Accession: T21587

K:Cottage, A:

Submitted to the EMBL Data Library, March 1997

A:Reference number: 219446

A:Accession: T21587

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 2;
Pred. No. 0.36;
0; Mismatches
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A; Introns: 18/3; 81/3; 133/1; 162/3; 181/1; 209/3
A; Note: F21F14.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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88.9%;
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-260 <CHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-204 <WIL>
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77 KFHRVIADE 85
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A;Gene: CESP:F31C3.1
2 FHRVIKDF 9
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55 FHRIIKDF
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A; Introns: 69/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-371 < PAD)
A; Residues: 1-371 < PAD)
A; Cross-rences: 1-371 < PAD)
A; Title: 1-343-552, 1996
A; Title: 1-343-552, 1996
A; Reference number: 571742; MUID:97027304
A; Recession: 571742
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                                                                                                                                                                                                                                               cyclophilin-like protein CPR6 - yeast (Saccharomyces cerevisiae)
NiAlternate names: protein L8167.24; protein YLR216c
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 24-Sep-1999
C;Accession: S48567; S71742
submitted to the EMBL Data Library, September 1994
A;Bescription: The sequence of S. cerevisiae cosmid 8167.
A;Reference number: S48545
A;Accession: S48567
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100.0%; Pred. No. 0.43;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: SGD:CPR6; CYP40
A;Cross-references: SGD:S0004206; MIPS:YLR216c
A;Map position: 12R
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Best Local Similarity 100.
Matches 8; Conservative
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A; Residues: 1-371 <DUI>
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89 FHRVIKDF 96
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                                2 FHRVIKDF
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A:Cross-references: EMBL:U40763; NID:g1117967; PIDN:AAB40347.1; PID:g1117968
A:Experimental source: thymus
A:Note: submitted to the EMBL Data Library, November 1995
C:Comment: This protein contains a cyclophilin-related domain, two 140K nuclear phosphop splicing by binding to splicing factors containing serine-arginine repeats protein.
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A;Accession: CB4777
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                  CC5314
CDC28/cdc2-like kinase associating arginine-serine cyclophillin - human
N/Alternate names: CARS-Cyp
N/Alternate names: CARS-Cyp
C.Species: Homo sapiens (man)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C.Accession: JC5314, GO2262
Gne 180, 151-155, 1996
A.Title: RS cyclophillins: Identification of an NK-TR1-related cyclophilin.
A.Reference number: JC5314; MUID:97128820
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Pred. No. 0.46;
2; Mismatches 0; Indels
            DB 2; Length 260;
                                                                                            0; Indels
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A;Amp position: 2
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
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A;Gene: GDB:CYP; CARS-CYP
A;Gene: GDB:CYP; CARS-CYP
C;Superfamily: CARS cyclophilin; cyclophilin homology
F;7-177/Domain: cyclophilin homology
                                                                                   1; Mismatches
        Score 43;
Pred. No. (
        87.8%;
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87.58;
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75.0%;
Query Match 87.8
Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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A; Residues: 1-754 <NES>
                                                                                                                                                                                                             144 FHRIIKDF 151
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65 FHRVVKDF 72
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Search completed: January 15, 2002, 13:06:15 Job time: 226 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

January 15, 2002, 13:04:04 ; Search time 24.88 Seconds (without alignments) 13.263 Million cell updates/sec

US-09-720-469-1 49 1 KFHRVIKDF 9 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ptio	P24367 qallus qall	1 bos tau	4 homo	m snm 6	7 homo	8 caeno	_	'n	_	P52013 caenorhabdi	P34791 arabidopsis		-	P52014 caenorhabdi	Q27450 brugia mala	_	P14832 saccharomyc	000060 uromyces fa	Q06118 streptomyce		P52015 caenorhabdi	P34790 arabidopsis	P52009 caenorhabdi	P47103 saccharomyc	P48820 bos taurus	5 mus π	P30414 homo sapien	2 homo	P52017 caenorhabdi	P52011 caenorhabdi	7.1	P52016 caenorhabdi	537
SUMMARIES	. OI	CYPB_CHICK	CYPB_BOVIN	CYPB_HUMAN	CYPB_MOUSE	CYPC_HUMAN	CYPB_CAEEL	CYPC_MOUSE	PPIB_TREPA	CYP6_YEAST	CYP5_CAEEL	CYP4_ARATH	CYPB_RAT	CYP4_CAEEL	CYP6_CAEEL	CYP1_BRUMA	CYP2_SCHPO	CYPH_YEAST	CYPH_UROFA	PPI_STRCH		CYP7_CAEEL	CYP1_ARATH	CYP1_CAEEL	CYP7_YEAST	RBP2_BOVIN	NKCR_MOUSE	NKCR_HUMAN	RBP2_HUMAN	CYPA_CAEEL	CYP3_CAEEL	CYPC_YEAST	CYP8_CAEEL	CYP9_CAFEL
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	Q08752 homo sapien					~	P05374 saccharomyc			=	.0
CYP4_BOVIN	CYP4_HUMAN	CYPH_ECHGR	CYPH_BLAGE	TP6A_AERPE	CYPH_MAIZE	CYPE_DROME	PEM1_YEAST	CYPH_DROME	CYPH_LUPLU	PPIA_MYCTU	PPIA_ACICA
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370	370	161	164	385	172	300	869	165	172	182	188
73.5	73.5	71.4	71.4	71.4	69.4	69.4	69.4	67.3	67.3	67.3	67.3
36	36	32	35	35	34	34	34	33	33	33	33
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	207 AA.		update) on update)	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)	HILLN) (SCILP).	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;					Cyclophilin tamily associated with		-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.	SOMERICALION OF PROLING IMIDIC	ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.	SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).	JERININ-TIPE FFIASE FAMILY.	This SWISS-PROT entry is copyright. It is produced through a collaboration	between the Swiss Institute of Bioinformatics and the EMBL outstation -	dong as its content is in no way	modified and this statement is not removed. Usage by and for commercial	entries requires a incense agreement (see nttp://www.isb-sib.cn/announce/ or send an email to license@isb-sib.ch).							Signal: Endoplasmic reticulum:		BY SIMILARITY. PEPTIDYL-PROLYL CIS-TRANS ISOMERASE R		SIMILARITY
	PRT;	reated)	 Last sequence update) Last annotation update) 	IS ISOMERASE	(a-cicio)	data; Crania	nathae; Galli				McGlynn E	to are of	1-10742(1991)	CELERATE THE	GOPEPTIDES.	YCLOSPORIN A	I: ENDOPLASMI	TO THE CICE	copyright.	tute of Bioi	by non-profit institutions as long	ent is not r	anse agreemen ense@isb-sib.				PPIase,	MRASE, L.	IASE_1; 1.	Rotamase: Si		BY SIMI PEPTIDY	PREVENT	(BY SIN
	STANDARD;	(Rel. 21, Cr	(Rel. 21, La (Rel. 38, La	CVCLODHILL	Cichoratrik	letazoa; Choi	Aves; Neogr	031;	N N	0364; PubMec	tothenfluh A	y pathway.";	m. 266:10739	I: PPIASES AC	PEPTIDE BONDS IN OLIGOPEPTIDES,	EGULATION: C	LAR LOCATION	TI. DELONGS	ROT entry is	Swiss Insti	-profit ins	this staten	mail to lice		, AAA49004	, 1CYN.	R002130; CS/	153; CSAPPIS	0170; CSA_PF	Isomerase;	mily.	1 24 25 207		
CT 1	ID CYPB_CHICK	P24367; 01-MAR-1992	15-JUL-1999	PEPTIDYL-PRO	Gallus gallus (Chicken).	Eukaryota; M	Archosauria;	Gallus. NCBI_TaxID=9031;	[1] SEOTENCE EDOM N.A.	MEDLINE-91250364; Pubmed-2040593;	Caroni P., Rothenfluh A., McGlynn "S.coolonbilin New member of the	the secretory pathway.";	J. Biol. Che	-!- FUNCTION	PEPTIDE		-!- SUBCELLU	TAPATATO	This SWISS-P	between the	use by non	modified and	or send an el		EMBL; M03333; AAA49004.1; DIR. AA0516. AA0516	HSSP; P23284; 1CYN.	InterPro; IPR002130; CSA_PPIase	PRINTS: PRO0153: CSAPPTSMRASE	PROSITE; PS00170; CSA_PPIASE_1;	Cyclosporin; Isomerase: Rotamase:	Multigene family	SIGNAL		
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Gaps

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Query Match

100.0%; Score 49; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels

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RESULT 3
CYPB_HUMAN
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                                                                                                                                                                                                                                                  01-0UN-1994 (Rel. 29, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PEPTIDIL-PROLYL CIS-TRAN ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Galat A., Bouet F.; "Cyclobiline B is an abundant protein whose conformation is similar to cyclobilin.A."; FEBS Lett. 347:31-36(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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PREVENT SECRETION FROM ER.
K -> G (IN REF. 3).
0097C88289AF6276 CRC64;
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Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94280416; PubMed-8010972; MecKe M.; Freedman R.B.; Tredenan R.B.; Trending R.B.; Trans-isomerase from the endoplasmic-reticulum lumen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 House A.K., Ratajczak T.;
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                  208 AA.
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PRINTS; PR00153; CSAPPISMRASE_1: PROSITE; PS00170; CSA_PPIASE_1: 1.
PROSITE; PS500770; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94283623; PubMed-8013656;
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22701 MW;
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                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
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208 AA;
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199
1 KFHRVIKDF
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ACYPB_BOVIN

ACYPB_BOTON

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ACYPB_BOTON

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Length 208;

DB 1;

100.0%; Score 49;

Query Match

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MEDLINE-92112948; Pubmed-1530944; Arber S., Krause K.-H., Caronl P.; "S-cyclophilin is retained intracellularly via a unique COOH-terminal sequence and colocalizes with the calcium storage protein calreticulin.";
                                                                                                                                                                                                                                   01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
EPETIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
                                  Gaps
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"Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-
prolyl isomerase with a signal sequence.";
Proc. Natl. Acad. Sci. U.S.A. 88:1903-1907(1991),
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SEQUENCE FROM N.A.

BOLLINE-2155036: PubMed-2040592;

Spik G., Haendler B., Delmas O., Mariller C., Chamoux M., Maes P.,

Tartar A., Montreuil J., Stedman K., Kocher H.P., Keller R.,

Tartar A., Movva N.R.;

"A novel secreted cyclophilin-like protein (SCYLP).";

J. Biol. Chem. 266:10735-10738(1991).
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-i- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-i- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-i- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
-i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mikol V, Kallen J., Walkinshaw M.D.,
"X-ray structure of a cyclophilin B/cyclosporin complex: compair, cyclophilin A and delineation of its calcineurin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 26-40.
MEDLINE-91156714; PubMed=2000394;
Price E.R., Zydowsky L.D., Jin M., Hunter C.H., McKeon F.D.,
                                  Indels
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BEDLINE-91260697; Pubmed-1710767;
Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;
"An endoptasmic reticulum-specific cyclophilin.";
Pred. No. 0.015;
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MEDLINE=93162043; PubMed=1286667;
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               Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                       sapiens (Human)
                                                                                                      84 KFHRVIKDF 92
                                                                     1 KFHRVIKDF 9
                                                                                                                                                                                                                                                                                                                                      PPIB OR CYPB.
                                                                                                                                                                                                      CYPB_HUMAN
P23284;
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SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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208
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PIR; S21835; S21835.
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Matches 9; Conser
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P45877;
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                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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01-MAR-1992 (Rel. 21, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-SI).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PREVENT SECRETION FROM ER. A814481B7EBD4579 CRC64;
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002130; CSA_PPIase.
Pfam: PF00160; pro_isomerase: 1.
PRINTS; PR00153; CSAPPISKRASE.
PROSTIE: PS00170; CSA_PPIASE_1: 1.
PROSTIE: PS50072; CSA_PPIASE_2: 1.
Cyclosporin: Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family: 3D-structure.
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-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY
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Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;
"An endoplasmic reticulum-specific cyclophilin.";
Mol. Cell. Biol. 11:3484-3491(1991).
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EMBL; M60477; AAA35733.1; -
PIR; A39118; CSHUB.
PIR; A40515; A40515.
PDB; ICYN; 29-JAN-96.
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22742 MW;
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Best Local Similarity
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SEQUENCE FROM N.A.
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P24369;
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CYPB_MOUSE
CYPB_MOUSE
DY 01.WARD
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAWASE)
(CYCLOPHILIN C).
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Zurini M.G., Quesniaux V.F., Movva N.R.;
"Human cyclophilin C: primary structure, tissue distribution, and
determination of binding specificity for cyclosporins.";
Biochemistry 33:8218-8224(1994).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
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-!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 49; DB 1; Length 208; 100.0%; Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4BBDF5AE40BAD3A7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP: P23284; ICYN.
MGD: MGT: 97750; Ppib.
InterPor: 1PR002130; CSA_PPIase.
Pfam; PP00160; Pro_isomerase; 1.
PRINTS; PR00153; CSA_PPISMRASE.
PROSTE; PS00173; CSA_PPIASE_1; 1.
PROSTE; PS00172; CSA_PPIASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94304830; PubMed-8031755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22713 MW;
                                                                                                                                                                                                                                                                                                        EMBL; M60456; AAA37498.1; -. EMBL; X58990; CAA41736.1; -.
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PPIC OR CYPC.
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                                                                                                                                                                                                                                                                                                                                     CYPC_MOUSE
P30412;
  Isomerase;
SEQUENCE
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                                                                                                                                                                                                                                                                                                                CYPC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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  (See http://www.isb-sib.ch/announce/
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-66276416; Pubmed-8694762; Page A.P., Macniven K., Hengartner M.O.; Facloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans."; Biochem. J. 317:179-185(1996).
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--- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
--- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
--- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 11 (EC 5.2.1.8) (PPIASE)
                                                                                                                                                                                                                                                                                                                                     100.0%; Score 49; DB 1; Length 212; 100.0%; Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                 Pfan: PF00160; pro_isomerase: 1.
PRINTS: PR00153; CSAPPISMRASE.
PROSTTE; PS00170; CSA_PPIASE_1; 1.
PROSTTE; PS50072; CSA_PPIASE_2; 1.
Cyclosporin; Isomerase; Rotamase; Multigene family.
SEQUENCE 212 AA; 22763 MW; 6F3DB547A2AE581B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 AA
                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
entities requires a license agreement (
or send an email to license@isb-sib.ch)
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EMBL; 266499; CAA91297.1; -.
HSSP, P05092; 3CYS.
WOTUMPEP; T01B7, 4; CE03588.
InterPro, IPR002130; CSA_PPIASE.
Ffam; PP00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPIASE.
PROSITE; PS00170; CSA_PPIASE.].
PROSITE; PS500772; CSA_PPIASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                         interpro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ROTAMASE) (CYCLOPHILIN-11).
CYP-11 OR TO1B7.4.
                                                        EMBL; S71018; AAB31350.1; -. HSSP; P05092; 2RMC.
MIM; 123842; -.
                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity luv...
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              1 KFHRVIKDF 9
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P52018;
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CYPB_CAREL

10 CYPB_CAREL

OT 01-0CT

DT 01-0CT

DT 01-0CT

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DE PEPTIND

DE ROTAMIN

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or send an email to license@isb-sib.ch),
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01-APR-1993 (Rel. 25, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN C).
                                                                                                                                                                                                                                                                                                                       Gaps
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Cell 66:799-806(1991).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOREPTIDES.
-!- ENZYME REGULETION: CYCLOSPORIN CSA) INHIBITS CYPC.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                 Length 183;
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MGD; MGI:97751; PPic.

InterPro; IPRO2130; CSA_PPIASE.

Pfam; PF00160; pro_1somerase; 1.

PRINTS; PR00153; CSAPPISMRASE.

PROSITE; PS00170; CSA_PPIASE_1; 1.

PROSITE; PS0072; CSA_PPIASE_2; 1.

Cyclosporin; Isomerase; Rotamase; Multigene family.

SEQUENCE 212 AA; 22794 MW; C99E7AA5D0FA04B6 CRC64;
Rotamase; Multigene family.
183 AA; 20193 MW; 23549C922828C533 CRC64;
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                                                                                                                                                                                                            89.8%; Score 44; DB 1; 100.0%; Pred. No. 0.12;
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                                                                                                                                                      Query Match
Best Local Similarity 100...
Era 8; Conservative
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Matches 8; Conservative
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|87 FHRVIKDF
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PPIB_TREPA

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Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE CPR6 (EC 5.2.1.8) (PPIASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00160; pro_isomerase; 1.
Pfam; PF00515; TPR; 1.
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InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U48867; AAC49414.1; -. EMBL; U14913; AAB67445.1; -.
                                                                                         CPR6 OR YLR216C OR L8167.24
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Best Local Similarity 100.
Matches 8; Conservative
01-OCT-1996 (Rel. 34, 01-OCT-1996 (Rel. 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P05092; 1AWV. SGD; S0004206; CPR6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isomerase; Rotamase
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                                                                                                                                                                  NCBI_TaxID=4932;
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                                                                          (ROTAMASE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                         "Identification of homologs for thioredoxin, peptidyl prolyl cis-trans isomerase, and glycerophosphodiester phosphodiesterase in outer membrane fractions from Treponema pallidum, the syphilis spirochete."; Infect. Immun. 65:4179-4180(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Proser C.M., North S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodesgren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                       Shevchenko D.V., Akins D.R., Robinson E.J., Li M., Shevchenko O.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.2.1.8) (PPIASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.8%; Score 44; DB 1; Length 215; 100.0%; Pred. No. 0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isomerase; Rotamase; Complete proteome.
SEQUENCE 215 AA; 23272 MW; CCA1589C1F5A6D0B CRC64;
                                                                                                                                                               Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                       20-AUG-2001 (Rel. 40, Last annotation update) PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC
                  215 AA
                                                                     (Rel. 37, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. NO. v...
                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE-97461344; PubMed-9317025;
                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-NICHOLS;
MEDLINE-98332770; PubMed-9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
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                                                      (Rel. 37, Created)
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                  STANDARD;
                                                                                                                                   (ROIAMASE).
PPIB OR PPI OR TP0947.
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                  NCBI_TaxID-160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hatch B., Hol
Venter J.C.;
                                                    15-DEC-1998
                                                                       15-DEC-1998
              PPIB_TREPA
066105;
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CYP6_YEAST
ID CYP6_YI
AC P53691;
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=S288C / AB972;

STRAIN=S288C / AB972;

A Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,

A Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,

Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,

Johnson D., Johnston L., Langston Y., Latreille P., Mardis E.,

A Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rifken L.,

A Miles L., Taich S., Trevaskis E., Vaudin M., Vignati D.,

A Miles L., Wilson R., Wohldman P., Waterston R.;

Submitted (SEP-1949) to the Embl.Genbank/DbBJ databases.

-! CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

C PETIDE BONDS IN OLIGOPEPTIDES.

-! SUBMITT: INTERACTS WITH RPD3.

-! SUBMILY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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SEQUENCE FROM N.A.
MEDLINE=97027304; PubMed=8873448;
Duina A.A., Marsh J.A., Gaber R.F.;
Identification of two CyP-40-like cyclophilins in Saccharomyces cerevisiae, one of which is required for normal growth.";
Yeast 12:943-952(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 AA; 42072 MW; 188666D94866DDDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPIASE, CYCLOPHILIN-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.8%; Scc.
100.0%; Pred. No.
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PROSITE; PSO0170; CSA_PPIASE_1; FALSE_NEG.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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P52013;
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371 AA.

PRT;

STANDARD;

CYP6_YEAST P53691;

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FIGR;

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NCBI_TaxID-10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 5 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLORPLAST PRECURSOR
(EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids II; Brassicales: Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea.
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
MEDLINE-96276416; PubMed-8694762;
Page A.P., Macolven K., Hengartner M.O.;
"Cloning and biochemical characterization of the cyclophilin homologues from the free-11ving nematode Caenorhabditis elegans.";
Blochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-i- CATANTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-i- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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MEDLINE-94179146; PubMed-8132503;
Lippuner V., Chou I.T., Scott S.V., Ettinger W.F., Theg S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00166; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE: PS00070; CSA_PPIASE_1: 1.
PROSITE: PS0072; CSA_PPIASE_2: 1.
Isomerase: Rotamase; Multigene family.
SEQUENCE 204 AA; 22366 MW; 22ABB39AD1127BAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.8%; Score 43; DB 1;
88.9%; Pred. No. 0.21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002130; CSA_PPIase.
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Matches 8; Conservative
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                                                                                                                    Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P23284; 1CYN.
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                                                                                                                                                                                                                                      SEQUENCE FROM N. A.
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                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                        (CYCLOPHILIN-5).
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CYP4_ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-1992 (Rel. 21, Created)
01-WAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                 STRAIN=CV. COLUMBIA;
MEDLINE=98088013; Pubbed=9426607;
Chou I.T., Gasser C.S.;
"Characterization of the cyclophilin gene family of Arabidopsis thallana and phylogenetic analysis of Known cyclophilin proteins.";
Plant Mol. Biol. 35:873-892(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDYL-PROLYL CIS-TRANS ISOMERASE:
D412AECBB8A5A3B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyclosporin; Isomerase; Rotamase; Chloroplast; Transit peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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87.5%; Pred. No. 0.28;
tive 1; Mismatches
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cyclophilin from Arabidopsis thaliana.";
J. Biol. Chem. 269:7863-7868(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfan: PF00160; pro_isomerase; 1.
PROUTS; CAAPITSMRASE.
PROSITE: PS00170; CSA_PPTASE_1; 1.
PROSITE; PS50072; CSA_PPTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P23284; ICYN.
SWISS-2DPAGE; P34791; ARATH.
InterPro; IPR002130; CSA_PPIase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L14845; AAA20048.1; -. EMBL; U42724; AAB96831.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multigene family.
                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 FHRIIKDF 151
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Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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Best Local Similarity 77.8%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches
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NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96276416; Pubmed=8694762;
                                                                                                                                                                                                                                                                                                                     EMBL; U36187; AAC06337.1; -.
EMBL; Z36949; CAA85417.1; -.
EMBL; Z46935; CAA87053.1; -.
EMBL; Z46935; CAA87053.1; -.
EMBL; Z36949; CAA87053.1; -.
HSSP; Q27450; 1A58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
SMART; SM00504; Ubox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002130; CSA_PPIase.
InterPro; IPR003613; Ubox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ROTAMASE) (CYCLOPHILIN-6).
CYP-6 OR F42G9.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       WormPep; F59E10.2; CE01596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
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320 KFHRLIKNF 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KFHRVIKDF 9
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CYP6_CAEEL
ID CYP6_CAEEL
AC P52014;
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                                                                                                                              PREVISIONS TO C-TERMINUS.

**REDLINE-92112948; PubMed-1530944;

**A REDLINE-92112948; PubMed-1530944;

**A PEDER S., Krause K.-H., Caroni P.;

**Rescyclophilin is retained intracellularly via a unique COOH-terminal structurin...*;

**T. Sequence and colocalizes with the calcium storage protein calreticulin...*;

**T. Call Biol. 116:113-125(1992);

**C. -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

**C. -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGORPHILIDES.

**C. -!- CATALYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.

**C. -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).

**C. -!- SIMELEMATRY: PARE PAREONS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYP4_CAEEL STANDARD; PRT; 523 AA. P52012; 009548; 01-0CT-1996 (Rel. 34, Last sequence update) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) PEPTIDYL,-PROLYL CIS-TRANS ISOMERASE 4 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page A.P., Macniven K., Hengartner M.O.; "Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans."; Biochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B. PREVENT SECRETION FROM ER
SEQUENCE FROM N.A.
MEDLINE=90300692; Pubwed=2194066;
Iwai N., Inagami T.;
"Molecular cloning of a complementary DNA to rat cyclophilin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
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76D12AC3427FEF32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PFIASE_2; 1.
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MEDLINE-96276416; Pubmed-8694762;
                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P23284; 1CYN.
InterPro; IPR002130; CSA_PPIase.
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208
208
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84 KFHHMIKDF 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KFHRVIKDF 9
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SIGNAL

5

RESULT 13
CYP4_CAEEL

TO YAPE
AC CYP4_CAEEL

DT 01-0CT
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 01-0CT
OC CYP-4
OC CYP

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01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 6 PRECURSOR (EC 5.2.1.8) (PPIASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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Cloning and biochemical characterization of the cyclophilin
homologues from the free-living nematode Caenorhabditis elegans.";
Biochem. J. 317:179-185(1996).
STRAIN=BRISTOL N2;
Subinbure J., Palmer S.;
Subintted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALTICA CTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1,
ISOMERASE; ROTAMASE; Multigene family.
SEQUENCE 523 AA: 58533 MW; 399967A6303989DE CRC64;
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Search completed: January 15, 2002, 13:14:58
Job time: 654 sec
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                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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027450.

15-JUL-1998 (Rel. 36, Last sequence update)

15-JUL-1998 (Rel. 36, Last sequence update)

20-AUC-2001 (Rel. 40, Last annotation update)

PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS

ISOMERASE) (CYCLOPHILIN) (PPIASE).
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MEDLINE-98318040; PubMed-9655334;
Mikol V., Ma D., Carlow C.K.S.;
"Crystal structure of the cyclophilin-like domain from the parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
NCBL_TaxID=6279;
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MEDLINE-98218582; PubMed-9559680;
Taylor P., Page A.P., Kontopidis G., Husi H., Walkinshaw M.D.;
The X-ray structure of a divergent cyclophilin from the nematode paraelte Brugia malayi.";
FEBS Lett. 425:361-366(1998).
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PEPTIDE BONDS IN OLIGOPEPTIDES.
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MEDLINE-96009642: PubMed-7547885;
Page A.P., Landry D., Wilson G.G., Carlow C.K.S.;
Page A.P., Landry D., Wilson G.G., Carlow C.K.S.;
Cyclophilin from the parasitic nematode Brugia malayl.";
Biochemistry 34:11545-11550(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.6%; Score 40; DB 1; Length 201 77.8%; Pred. No. 0.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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InterPro: IPR002130; CSA_PPIASE.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_2; 1.
ISOMERASE; ROLAMASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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Protein Sci. 7:1310-1316(1998).
[4]
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                                                                                                                                                                                                                                                                                        EMBL; U27354; AAC47124.1; -. EMBL; U00051; AAA91355.1; -. HSSP; P23284; ICYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 AA;
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SEQUENCE
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                                                                                                                    Biochemistry 39:592-598(2000).
--- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
--- ENZYME REGULATION: RELATIVELY INSENSITIVE TO INHIBITION BY CSA.
--- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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               MEDLINE-20108543; Pubmed-10642184;
Ellis P.J., Carlow C.K.S., Ma D., Kuhn P.;
"Crystal structure of the complex of brugia malayi cyclophilin and
cyclosporin A.";
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X-RAY CRYSTALLOGRAPHY (2.47 ANGSTROMS) OF 1-177.
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Pred. No. 5.6;
L; Mismatches
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Pfam; PP00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1: 1.
PROSITE; PS50072; CSA_PPIASE_2: 1.
PROSITE; PS6072; CSA_PPIASE_2: 1.
DOMAIN 10 175
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ilarity 87.5%;
Conservative
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Best Local Similarity
7; Conserv
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Search time 78.85 Seconds
(without alignments)
16.696 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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                                                                                                January 15, 2002, 13:05:29
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Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
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3: sp_fungi:*
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sp_vertebrate:*
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49
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	001490 orbinomyces	O88541 rattus norv	O9bvk5 homo sapien	Ogdcv1 mus musculu	O9v3c6 homo sanien	Ogdows miscuria	O9w227 drosophila	O98ue5 xenona) ae	O9zvi4 arabidonsis	Ogato5 vancheria)	015729 entamoeba h	O9fw22 orvza sativ	043447 homo sapien	09cau7 mus musculu	09v9b9 drosophila	ulusum sum 89860	09zra9 pseudotsuga	Oguéus plasmodium	027716 plasmodium
SUMMARIES	σī	001490	088541	Q9BVK5	Q9DCY1	09Y3C6	Q9D0W5	09W227	098UE5	092VJ4	09ATC5	015729	Q9FW22	043447	09COU7	09V9B9	090868	Q9ZRQ9	09u6u5	927716
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094190 emericella 093826 trichophyto 070134 mus musculu 09vaw2 drosophila 099p41 echinococcu 09ch46 lactococcus 095th5 arabidopsis 062190 caenorhabdi 099qu0 oryza sativ 09fph5 arabidopsis 055035 rattus norv 013427 homo sapien 09vaw1 drosophila 09vaw1 drosophila 09sw1 drosophila 09sih1 arabidopsis 09sib1 arabidopsis 09f998 arabidopsis 09f998 arabidopsis 076826 caenorhabdi 076826 caenorhabdi 076826 caenorhabdi 076826 onchocerca 061300 dirofilaria 09w0q2 drosophila 076944 staphylococ 096877 onchocerca	IENTS	PRT; 203 AA. , Created) , Last sequence update) , Last annotation update) , Last annotation update.	Neocallimasticales;	RA (1) RA MEDLINE=95223986; PubMed=7708690; RA Chen H., Li XL., Ljungdahl L.G.; "A cyclophilin from the polycentric anaerobic rumen fungus Orpinomyces RT SP, strain PC-2 is highly homologous to vertebrate cyclophilin B."; RI Proc. Natl. Acad. Sci. U.S.A. 92:2587-2591(1995). CC -i- FUNCTION: PPIRASES ACCELERATE THE FOLDING OF PROTEINS. CC -i- CATALYIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC	(CSA) INHIBITS CYPB. RETICULUM LUMEN (BY SIMILARITY). HILIN-TYPE PPIASE FAMILY.		PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B. CSA (POTENTIAL). PREVENT SECRETION FROM ER (BY SIMILARITY). A5748C94305B8BE0 CRC64;
094190 093826 070134 090VAW2 095P41 095P41 095P190 095S191 095S191 095S191 095S191 095S191 0976824 0976824 0976824 0976824 0976824 0976824 0976824 0976824 0976824 0976924	ALIGNMENTS	PRT; Created) Last sequ Last anno	tridiomycota; Ne Orpinomyces.	JENCE OF 3 18690; L.G.; reentric employeds n. 92:2587 3RATE THE	PTIDES. SPORIN A IDOPLASMIC	86. ase. :: 1. E. :_1; 1. Cyclospc	PEPTIDYI CSA (POT PREVENT SIMILARI
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Length 216;

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23742 MW; 2D0410A07AA9E420 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 18, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN B (EC 5.2.1.8).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
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"Unilgight to the EMBL/GenBank/DDBJ databases.

"In EUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).

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"IN OLIGOPEPTIDES.

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"IN OLIGOPEPTIDES.

"IN TANNS ISOMERASE FAMILY.

"EMBL. REPAIDYL-PROLYL CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDALARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.

"EMBL. ARCASS90.1; "...
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B).
HOMO Sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                           100.0%; Score 49; DB 3; Length 203; 100.0%; Pred. No. 0.066; 1ive 0; Mismatches 0; Indels
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TISSUE-SKIN, AND MELANOMA;
Strausberg R.;
Stubmitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMPL; BC001125; AAH01125.1;
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STRAIN-WISTAR-KYOTO; TISSUE-KIDNEY;
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Pfam: PF00160; pro_isomerase; 1.
PROSITE; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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STRAIN=C57BL/6J; TISSUE=KIDNEY;

KRAMIS-C57BL/6J; TISSUE=KIDNEY;

KRAMIS-C57BL/6J; TISSUE=KIDNEY;

KRAMIS J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Radawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.S., Salto K., Desole G., Quackenbush J.,

Kadota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazarelli J., Momberts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamcto N.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamcto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Norshaw-Borits A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havachizaki V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 49; DB 11; Length 216; 100.0%; Pred. No. 0.071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CE9DAD1544AE72FE CRC64;
                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: AK002357; BAB22036.1; -. MGD: MGI: MCI: 97750; Ppib. InterPort: 17750; Ppib. Pfam: PF00160; Pro_isomerase: 1. PRNINTS; PR00153; CSAPPISMRASE. PROSITE: PS50072; CSAPPISMRASE. SEQUENCE 216 AA; 23713 MW; CE9D.
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0
                                                         01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                           PEPTIDYLPROLYL ISOMERASE B.
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Best Local Similarity luv...
9; Conservative
PRELIMINARY;
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m

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SEQUENCE
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                            QQ
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MEDLINE-21085660; PutHed-11217851;

ARAN J., Shibadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Baito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Gissi C., King B., Kochiwa H.,

Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okkido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin W.-C.; "Comparative gene cloning: Identification of novel human genes with Caenorhabditis elegans protecome as template."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 AA; 18237 MW; 2872DC3336CD05E4 CRC64;
01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CGI-124 PROTEIN (EC 5.2.1.8).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P05092; 2RMC.
InterPro; IPR002130; CSA_PPIase.
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Best Local Similarity 88.9.
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||:||||
52 KFHRIIKDF 60
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                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KFHRVIKDF 9
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RY SEQUENCE FOR NA. 6.

RY Addams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RA Addams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RA Addams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortunen J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Fandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Han K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Hall J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Bellew R.M., Basu A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davonport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davonport L.B., Davies P.,

RA Cherry J.M., Evangelista C.C., Ferriac S., Fleischmann W.,

RA Dodson K.J., Evangelista C.C., Ferriac S., Fleischmann M.,

RA Goods R., Gorrell J.H., Guz J., Gurn P., Harris M.,

RA Horstin D., Houston K.A., Howland T.J., Wei M.-H., Ibbeywam C.,

RA Jalali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., King B., Ringwald M., Rodriguez T., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Borris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea: Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001).

-!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                    Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last annc
CG2852 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS500170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1916066; 1110060010Rik.
InterPro: 1PR0002130; CSA_PPDase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AK004331; BAB23265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isomerase; Rotamase.
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52 KFHRIIKDF 60
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89.8%;
100.0%;
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Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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                                              1 KFHRVIKDF
                                                                                                                   84 KFHRVIKEF
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SEQUENCE
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SEQUENCE
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Kimmel B.E., Kodira C.D., Kraft C., Kravitž S., Kulp D., Lai Z., Liang Y., Lin X., Lauk X., Mattel B.B., McIntosh T.C., McLood M.P., Morpherson D., Merkulov G., Milshina N.V., Mobary C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Molson B.R., Nalson K.A., Nixon K., Nussken D.R., Packel J.M., Pittnan G.S., Pan S., Pollard J., Puri V., Resse M.G., Palazzolo M., Pittnan G.S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shee B.C., Siden-Klamos I., Simpson M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Sylest E., Spradling A.C., Stapleton M., Strong R., Wang Z., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhang F.N., Zhan W., Zhang X., Zhu X., Smith H.O., Globs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Science 287:2185-2195(2000)

C. I. CATALITIC ALTIVITIC SINILLERITY)

C. I. CATALITIC SINILLERITY)
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Amano T., Yoshizato K.;
"Isolation of genes involved in intestinal remodeling during anuran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE BONDS IN OLIGOPEPTIDES.
--- SMILARITY: BELEVANS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE PAMPA TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS, ISOMERASE, AAF46873.1; -.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROLNE LIS-TRANS ISOMERASE B (FRAGMENT).
Xenopus laevis (African clawed frog).
Amphibia: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia: Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.0%; Score 48; DB 5; Length 205; 88.9%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 104
104 AA: 11350 MW; BF6AD1CD1C2FB3E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22199 MW; A9CEF88BICC813F7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE. PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P23284; ICYN.
FlyBase; FBgn0034753; CG2852.
InterPro; IPR002130; CSA_PPIase.
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 88.9 Matches 8; Conservative
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77 KFHRIIKDF 85
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SEQUENCE
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudlcotyledons; core eudlcots; Rosidae;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; stramenopiles; Xanthophyceae; Vaucheriales; Vaucheriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
Arabidopais thaliana chromosome II BAC 76A23 genomic sequence.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005499; AAC67345.1;
HSSP; P05002; 2CPL.
Meddel; 38509; Arath;1040;38509.
InterPo: IPRO0130; CSA_PPIASE.
PFINTS; PRO0163; CSAPPISMRASE.
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                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
pUTATIVE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
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Pred. No. 0.39;
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Pred. No. 0.44;
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199 AA.
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Gaps

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Matches

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MEDLINE-98230239; PubMed-9570313; Teigelkamp S., Achsel T., Mundt C., Gothel S.F., Cronshagen U., Langew.S., Marahiel M., Luhrmann R.; "The 20kD protein of human [14/106.05] tri-snRNPs is a novel cyclophilin that forms a complex with the U4/106-specific 60kD and 90kD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M., Chen C.-S., Shaw J.-F.;
Chen C.-S., Shaw J.-F.;
"Oryza sativa PAC P0036D10 genomics sequence, complete sequence.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC073405; AAG03106.1; -.
EMBL; AC073405; DRAG03106.1; -.
PRINTS: PR00163; CSA_PPIASE.
PRINTS: PR00163; CSA_PPIASE.
PRINTS: PS50072: CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Horowitz D.S., Kobayashi R., Krainer A.R.; A new Cyclophilin and the human homologues of yeast Prp3 and Prp4 form a complex associated with U4/U6 snRNPs."; RNA 3:1374-1387(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                   89.8%; Score 44; DB 10; Length 173; 100.0%; Pred. No. 0.53; Live 0; Mismatches 0; Indels
                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
U-SNRNP-ASSOCIATED CYCLOPHILIN (EC 5.2.1.8).
USA-CYP OR CYP-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                    177 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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InterPro; IPR002130; CSA_PPIase.
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                                                                                                                                                                                                                                     Query Match 89.83
Best Local Similarity 100.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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TISSUE-CHORIOCARCINOMA;
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SEQUENCE FROM N.A.
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     Gaps
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Submitted (Nov-1997) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: PEPTIDYL-PROLY LISTRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-! CATALYTTC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOREPTIDES.
-! SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-PEMBL; AF017993; AAB86601.1; -. HSSP; P056092; 2CPL.
HSSP; P056092; 2CPL.
Interpro; INDR00130; CSA_PPIASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OJ-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 16, Last sequence update)
SIMILAR TO ARABIDOPSIS THALIANA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
(P34791) (FRAGMENT).
Oryza sativa (Rice).
Elkaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                       STRAIN-HMI:IMSS;
Carrero J.C., Petrossian P., Acosta-Camarena E., Ostoa-Saloma
Ortiz-Ortiz L., Laclette J.P.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.8%; Score 44; DB 5; Length 167, 100.0%; Pred. No. 0.51; O. Mismatches 0; Indels
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18139 MW; DBA23FE5BB3290B2 CRC64;
                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
   ö
                                                                                                                                                           167 AA.
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   Mismatches
                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                      Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00166; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Cr
01-JAN-1998 (TrEMBLrel. 05, La
01-JUN-2001 (TrEMBLrel. 17, La
CYCLOPHILIN (EC 5.2.1.8).
CYP1.
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                   33 FHRVIKDF 40
                                                                                                                                                                                                                                                                                                  Eukaryota; Entamo
NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||||||
55 FHRVIKDF 62
                                 2 FHRVIKDF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-HM1: IMSS;
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SEQUENCE

Query Match

09FW22;

RESULT
09 FW22
10 09 FW22
10 09 PT
00 0

Q9FW22 12

SEQUENCE

RESULT 11
015729
AC 015729
AC 015729
DT 01-JAN

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65 FHRVIKDF 72
 2 FHRVIKDF 9
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                     Q9V9B9
                                                                                                                                        Q9V9B9
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                                                                                    RESULT
09V9B9
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Ra Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Ra Arakawa T., Hara A., Eukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Aito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Ra Acdota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ra Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
Ra Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
Ra Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,
Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Ra Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Rons Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Ra Sasaki H., Sato K., Schoenbach C., Seya T., Sakamoto N.,
Ra Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
Whyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Wansachizaki V.
                                                                                      ö
                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOLDING OF PROTEINS (BY SIMILARITY).
                                                                                    ö
                                                  Length 177;
                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 AA; 19208 MW; 566BCE6361E0F339 CRC64;
177 AA; 19208 MW; 566BCE6361E0F339 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-HEAD, EMBRYO, AND CEREBELLUM;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
4833408FIIRIK PROTEIN (1100001J08RIK PROTEIN).
                                                  Score 44; DB 4;
Pred. No. 0.54;
                                    89.8%; Scur.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                               Created)
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PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1913351; 1100001008Rik.
MGD; MGI:1921150; 4833408F11Rik.
InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                  4833408F11RIK OR 1100001J08RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANS ISOMERASE FAMILY.
EMBL; ARO14665; BAB29493.1;
EMBL; ARO05179; BAB22623.1;
EMBL; ARO05202; BAB23880.1;
                                                                                                                                                                                                                                                            09CQU7;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
                                                Query Match 89.8
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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65 FHRVIKDF 72
                                                                                                                      2 FHRVIKDF 9
 SEQUENCE
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                                                                                                                                                                                                             RESULT 14
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Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., 11 P.W., Hoskins R.A., Galle R.F.,
Ra Amanatides P.G., Scherer S.E., 11 P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O. Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O. Chen L.X.,
Bandon R.C., Rogers Y.H.C., Halt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Apbayani A., An H.J., Andrews Pfennkoch C., Baddwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaslay E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bottlar P.,
Borkova D., Bottlann M.R., Bouck J., Bhandari D., Bottlar P.,
Borkova D., Bottlann M.R., Bouck J., Bhandari D., Dew I., Dietz S.M.,
RA Berlos B., Delcher A., Deng Z., Ways A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahnke C., Dewneport L.B., Daviss P.,
RA de Pablos B., Delcher A., Howley S., Chron C., Gans T., Dietz S.M.,
RA de Pablos B., Delcher A., Howley S., Conyel J.H., Guz S., Dunkov B.C., Dunn P.,
RA drifts N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Marvey D., Helman T.C., Mell M., Nollow N., Classor K.A.,
Jalali M., Kalush F., Karpen G. H., Kaz J., Keanison J.A., Kedinez C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., Wolder C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., Wolder M., Mirphy D., Muzny D.M., Nalson D.L.,
RA Mount S.M., Wooder R., Shen S., Pollard J., Purl V.,
Ra Riber B.C., Siden K.A., Williams Y., Wang D., Sun E.,
RA Shirskas R., Tector C., Turner R., Venter E., Sand H., Wang S., Yao Q.A.,
RA Reinert K., Remidgton K.A., Stappieco M., Strong R., Sun E.,
Ra Shirskas R., Tector C., Turner R., Venter E., Wang A., Wang Z.Y., Wang S. Then M., Wender S.M., Woodege T., Wolly W., Wellow D., Sun S., Shen G., Stappieco M., Wellow D., Wellow D., Sun S., Shen G., Shen R., Rubin G., Shen M., Sheng S., Sheng S., Sheng S., Sheng S., She
                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS50072; CSA_PPIASE_2; 1.
SEQUENCE 183 AA; 20182 MW; 19E5CE187CB9E949 CRC64;
                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
0.56;
183 AA.
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Pred. No.
                                         Created)
                                                                                                                                            Drosophila melanogaster (Fruit fly)
PRT;
                                                                                                                                                                                                                                                                                                              MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002130; CSA_PPIase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.8%;
100.0%;
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                                  01-MAY-2000 (TrEMBLEEL 13, 01-MAY-2000 (TrEMBLEEL 13, 01-JUN-2001 (TrEMBLEEL 17, CG17266 PROTEIN.
PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                         STRAIN-BERKELEY;
                                                                                                                                                                                                         Ephydroldea; Dr
NCBI_TaxID=7227
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Gaps

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Indels

.; 0

100.0%; Pred.

Conservative

Best Local Similarity Matches 8; Conserv

Query Match

89.8%; Score 44; DB 11; Length 177; 100.0%; Pred. No. 0.54;

; 0

0; Gaps

0; Indels		
ó		
0; Mismatches		13:16:24
0;		2002,
8; Conservative	2 FHRVIKDF 9 	Search completed: January 15, 2002, 13:16:24 Job time: 655 sec
Matches	0y 2 Db 71	Search completed: Job time: 655 sec

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January 15, 2002, 13:02:09; Search time 81.32 Seconds (Without alignments) . 8.198 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DMT.
/SIDSB/gcgdata/geneseq/geneseqp/AA1990.DMT.
/SIDSB/gcgdata/geneseqp/AA1991.DMT.
/SIDSB/gcgdata/geneseqp/AA1991.DMT.
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/SIDSB/gcgdata/geneseqp/AA1992.DMT.
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/SIDSB/gcgdata/geneseq/geneseqp/AA1994.DMT.
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| SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAN
| SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAN
| SIDSB/gcgdata/geneseqy/geneseqp/AA1983.DAN
| SIDSB/gcgdata/geneseqy/geneseqp/AA1984.DAN
| SIDSB/gcgdata/geneseqy/geneseqp/AA1986.DAN
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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49
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMAKIES		
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Result	1	Query					
2	Score	Match	e Match Length DB I	DB	ID	Description	u
	4	100.0	σ	21		Caro demin	100 b 4 1 4 5
7	4	100.0	σ	22	AAB46930	Cyclindan Cyclinda	lophilin
e	4	100.0		71	AAG00090	Human cyc	eyerophirin
4	49	100.0		22	AAB73302	Human one	leted pro
2	49	100.0		22	AAB73301	Himan Cyc	cyclophilin
9	49	100.0		21	AAB43878	Himan Cyc	TODE TOO
7	48	98.0		21	AAG03983	Himan con	cancer assuc
œ	48	98.0		22	AAU12175	Human SCO	7007
6	48	98.0	178	22	AAG75471	Human CO.	A sout POLY
10	46	93.9		21	AAY69962	Human CVD	Jone taller
11	46	93.9	σ	22	AAB46946	Human cyc	cyclophilin

Claim 4; Page 49; 64pp; Japanese

Human prostate can Cyclophilin C. Mu A. niger peptidyl- Arabidopsis thalia Arabidopsis thalia Arabidonsis thalia	a a a a a a a a a a a a a a a a a a a	bidops bidops bidops bidops mmitis mmitis	B. malayi cyclosph Yeast peptidyl-pro Yeast peptidyl pro Yeast peptidyl pro Arabidopsis thalia
AAB5670 AAR3235 AAY9204 AAG1646 AAG1646	AAB84 AAG37 AAG37 AAG11 AAG32 AAG32	AAB4913 AAB4913 AAB4913 AAB4913 AAB4913 AAB4913	AAR7 4292 AAR1 0764 AAR7 2262 AAR7 2918 AAG5 2015 AAG5 0214 AAG5 0214 AAG5 0213 AAG3 04 03
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25 25 25 26	901 112 114 114 144	2022222	589 162 162 163 163 173 172 172 173 193 193
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4 4 4 4 4 4 4 4 4 6 6 6 6	4444444 EUUUUUUU		, , , , , , , , , , , , , , , , , , ,
12 13 14 15 17	18 19 20 21 23 24 25	26 27 28 30 31 33 33	4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

ALIGNMENTS

Tumour antigen peptides derived from cyclophilin B for treatment and diagnosis of tumours $\,\cdot\,$ Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; Human cyclophilin B peptide fragment #1. HLA antigen; diagnosis; tumour; therapy AAY69921 standard; peptide; 9 AA. (SUMU) SUMITOMO PHARM CO LTD. (ITOH/) ITOH K. 99WO-JP03360, 98JP-0178449, 11-APR-2000 (first entry) WPI; 2000-116932/10. Itoh K, Gomi S; 24-JUN-1999; Homo sapiens W09967288-A1 25-JUN-1998; 29-DEC-1999. AAY69921; RESULT AAY69921 Length 9;

*88888 *8886 *8888 *888 *8888 *8888 *8888 *8888 *8888 *8888 *8888 *8888 *8888 *8888 *888 *888 *8880 *8880 *8880 *8880 *8880 *8880 *8880 *8800 *8800 *8800 *8000 *8

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Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                    AAG00090;
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                                                                                                                                AAG00090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes the novel use of interferons (IFNs) or DNAs capable of expressing the interferons and/or antigenic perteins (AP), antigenic peptides derived from the proteins or DNAs capable of expressing the antigenic proteins or peptides, in the manufacture of an agent for induction of antigen-specific T cells. The products of the invention have virucide and cytostatic activity and can be used for gene therapy or as inducers of antigen-specific T cells. The action of interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic T cell (CTL) by administering an antigenic peptide in an incomplete Freund's adjuvant (IFA) emulsion preparation form was evaluated IFNs (or DNA encoding IFNs) are useful in the manufacture of a medicament for administered with AP (or DNA encoding AP) or vice versa. The medicament is useful for the treatment or prophylaxis of a tumor or a viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of antigenic proteins, peptides, interferon or their encoding DNA, in the manufacture of an agent for the induction of antigen-specific T cells
              This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                              Tumor antigenic peptide; interferon; IFN; antigen-specific T cell; virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell; viral infectious disease; cyclophilin B; human.
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                                                                                                                                                                                                                                                                                                                                     Human cyclophilin B derived tumor antigenic peptide SEQ ID 16.
                                                                                                                  100.0%; Score 49; DB 21; Length 9; 100.0%; Pred. No. 4.3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 15; 25pp; English.
                                                                                                                                                                                                                                                            AAB46930 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamaoka T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUMU ) SUMITOMO PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUL-2000; 2000EP-0306263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0207687.
                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                              Conservative
                                                                                                         Query Match
Best Local Similarity
These 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-193144/20.
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                                                                                                                                                                      1 KFHRVIKDF 9
                                                                              9 AA;
                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' uptra is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic blass. 5' ESTs are also used in diagnostic, forensic, gene therapy and
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                                                             Gaps
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                                                       Indels
  Score 49; DB 22;
Pred. No. 4.3e+05;
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                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein, SEQ ID NO: 4171.
                                                                                                                                                                                                                                                                                                                    AAG00090 standard; Protein; 166 AA.
h
Similarity 100.0%;
9; Conservative 0;
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N-PSDB; AAC00096.
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                                                                                                                     1 KFHRVIKDF 9
                                                                                                                                                   (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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RESULT AAB73302

AAB73301 standard; protein; 216 AA.

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The invention relates to a composition for modulating somatolactogenic function, comprising cyclophilin B (CyBB), a mutant of cyclophilin B (Carticularly a CyBB mutant in which residues 2-12 of the mature protein are absent) or an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, and a method of inhibitors of somatolactogenic functions using CyPB and a somatolactogenic hormone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions by assessing CyPB and a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic function in the animal, and cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, is useful for inhibiting somatolactogenic function in the animal. A composition comprising cyclophilin B is useful in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B with a somatolactogenic composition comprising cyclophilin B mutant or a composition comprising cyclophilin and mutant or a cyclophilin and mutant or a cyclophilin and mutant or a cyclophilin cyclophilin cyclophilin and mutant or a cyclophilin cyclophilin cyclophilin and mutant cyclophilin cyclophilin and mutant cyclophilin cyclophilin cyclophilin cyclophilin cyclo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone
                                                                                                                                                                                                                              Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia; C-terminal deletion mutant; mutein.
                                                                                                                                                                              Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.
AAB73302 standard; protein; 211 AA.
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                                                                                                                    22-MAY-2001
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                                                             AAB73302
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'Match 100.0%; Score 49; DB 22; Length 211; Local Similarity 100.0%; Pred. No. 0.039; les 9; Conservative 0; Mismatches 0; Indels (
Query Match
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1 KFHRVIKDF 9

Matches

AAB73301 RESULT

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The Invention tetaters to a composition for modutating somatoractogenic function, comprising cyclophilin B (CypB), a mutant of cyclophilin B (CypB), a mutant of cyclophilin B (PypB) are absent) or an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone (e.g., prolactin, growth hormone). The invention also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic function in the animal, and cyclophilin B mutant or a composition comprising an inhibitor of thee interaction of cyclophilin B with a somatolactogenic hormone, is useful for inhibiting cyclophilin B with a somatolactogenic hormone, is useful in the treatment of immunosuppression, in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition of cyclophilin B mutant or a composition comprising cyclophilin B. Cantor or a composition comprising cyclophilin B. Cantor or a composition comprising cyclophilin B. Cantor or a composition comprising cancer, gigantism/aeromegally, and hyperperior cancer, gigantism/aeromegally. The present cancer 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to a composition for modulating somatolactogenic
                                                                                                                                                                                                                           somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia.
                                                                                                                                                                                                     Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-AUG-2000; 2000WO-US21789.
                                                                                                                                                     Human cyclophilin B (CypB).
                                                                                                22-MAY-2001 (first entry)
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Best Local Similarity 100.

Matches 9, Conservative
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                                                AAB73301;
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ID AAB4
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AC AAB4
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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dumas Milne Edwards J, Duclert A, Glordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; SEQ ID 8064; 71pp + CD-ROM; English.
                                                                                                                                                                                 Human secreted protein, SEQ ID NO: 8064.
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                           AAG03983 standard; Protein; 113 AA.
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Matches 8; Conservative
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N-PSDB; AAC03989.
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                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                          Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antichentalic; antirheumatic; antiarthritic; antivital; antiinflammatory; antithyroid; antialergic; antiarthritic; antivital; dermatchogical; neuroprotective; thrombolytic; cagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                               Human cancer associated protein sequence SEQ ID NO:1323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 1974-1975; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2000; 2000WO-US05882.
                           (first entry)
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Best Local Similarity | 100...
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA, Ruben SM;
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N-PSDB; AAC78087.
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|167 kfhrvikdf 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KFHRVIKDF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                             08-FEB-2001
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Human secretory and transmembrane; PRO; mammalian; cancer; lung;
breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
                                           ó
  DB 21; Length 113;
                                           0; Indels
Score 48; DB 21
Pred. No. 0.032;
1; Mismatches
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Sequence

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AAU12172-AAU12446 represent novel human secretory and transmembrane
PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bloactive molecules to cells expressing
PRO polypeptides, to modulate biological activities of cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
Dreast, prostate, rectal, cervical or liver tumours by comparing PRO
Dolypeptide expression in a cell sample to that in a control sample.
Come of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor alpha (TNF-alpha) from human blood, the
proliferation or differentiation of chondrocytes, the proliferation or
proliferation or differentiation of chondrocytes, the proliferation of
cartilage, the proliferation of inner ear utricular supporting cells or
Coff T-lymphocytes, the release of a cytokine from peripheral blood
Coff T-lymphocytes, the release of a cytokine from peripheral blood
Coff T-lymphocytes, the proliferation of endothelial cells. Some of
the PRO polypeptides may modulate glucose or free fatty acid uptake by
skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
Coff factor VIIA. The PRO polypeptides can be used in assays to identify
molecules involved in binding interactions. The polynucleotides encoding
cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deforge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Fig 8; 813pp; English.
                                                                                                                                                                                                                                                                   99US-0170262.
99WO-US30095.
99WO-US30911.
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2000WO-US15264.
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-408281/43.
N-PSDB; AAS21247.
                                                                                  WO200140466-A2.
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18 - FEB - 2000;

22 - FEB - 2000;

24 - FEB - 2000;

24 - FEB - 2000;

01 - MAR - 2000;

20 - MAR - 2000;

21 - MAR - 2000;
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20-DEC-1999;
20-DEC-1999;
30-DEC-1999;
06-JAN-2000;
06-JAN-2000;
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17-MAY-2000;
22-MAY-2000;
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02-JUN-2000;
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09-DEC-1999;
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                                                                                                                  07-JUN-2001
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens. The colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in the prevention, diagnosis and treatment of diseases associated with inappropriate postpression. For example, N and P may be used in the prevention, associated with decreased expression by rectifying mutations or deletions in a partient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. Co sypress the proteins N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                         Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma.
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0
                                                                                             Score 48; DB 22; Length 166;
Pred. No. 0.048;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                           Human colon cancer antigen protein SEQ ID NO:6235.
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                                                                                                                                                                                                                                                                         AAG75471 standard; Protein; 178 AA.
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                                                                                               98.0%;
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99US-0163280.
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                                                                                                                                                                                                                                                                                                                                         03-SEP-2001 (first entry)
                                                                            Ouery Match
Best Local Similarity 86.5.
For 8; Conservative
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                                                 Sequence 166 AA;
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                                                                                                                                                            1 KFHRVIKDF
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| 52 kfhriikdf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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178 AA;

Sequence

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WPI; 2001-193144/20
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infectious disease.
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Best Local Similarity
Matches B; Conserv
                                                                                                                                                                                                                                                                                                                            9 AA;
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                      Homo saplens
                                     EP1074267-A1
                                                                                   22-JUL-1999;
                                                     07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB56701;
                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                            in the
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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                                                                                                                                                                                                                                                                                                                                                           This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                      Tumour antigen peptides derived from cyclophilin B for treatment and
                       Gaps
                                                                                                                                                           Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
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     Score 48; DB 22; Length 178; Pred. No. 0.052;
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Pred. No. 4.3e+05;
1; Mismatches 0; Indels
                      0; Indels
                       1; Mismatches
                                                                                                                                             Human cyclophilin B peptide fragment #42.
                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 60; 64pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB46946 standard; peptide; 9 AA
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                                                                                                                                                                                                                                                                 (SUMU ) SUMITOMO PHARM CO LTD. (ITOH/) ITOH K.
                                                                                             AAY69962 standard; peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                           93.9%;
       98.0%;
88.9%;
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Ouery Match
Best Local Similarity 88.9,
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                              diagnosis of tumours
                                                                                                                                                                                                                                                                                                        WPI; 2000-116932/10.
                                               1 KFHRVIKDF 9
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                                       1 KFHRVIKDF 9
                                                                                                                                                                                                                                                                                         Itoh K, Gomi S;
                                                                                                                                                                                                                                                                                                                                                                                                    9 AA;
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| kyhrvikdf
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                                                                                                                            11-APR-2000
                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                   29-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                              AAY69962;
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                                                                                      AAY 69962
                                                                               RESULT
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XXEXEXXX
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This invention describes the novel use of interferons (IFNs) or DNAs capable of expressing the interferons and/or antigenic proteins (AP), antigenic peptides derived from the proteins or DNAs capable of expressing the antigenic proteins or DNAs capable of expressing the antigenic proteins or peptides, in the manufacture of an agent for induction of antigen-specific T cells. The products of the invention have virucide and cytostatic activity and can be used for gane therapy or as inducers of antigen-specific T cells. The action of interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic T cell (CTL) by administering an antigenic peptide in an incomplete Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or DNA encoding IFNs) are useful in the manufacture of a medicament for inducing antigen-specific T cells in an individual who has been administered with AP (or DNA encoding AP) or vice versa. The medicament of the or the treatment or prophylaxis of a tumor or a viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antlinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of antigenic proteins, peptides, interferon or their encoding DNA, in the manufacture of an agent for the induction of antigen-specific {\bf T}
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virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell; viral infectious disease; cyclophilln B; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Pred. No. 4.3e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rakasu H, Gotoh M, Yamaoka T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SUMU ) SUMITOMO PHARM CO LTD.
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WO200018934-A1
              Friedman JS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY92048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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    δ
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                                                                                                                                                                                                                                     AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                       Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclophilin C; bone marrow; stromal cell line; AC 6; interleukin-1; IL-1; cyp A; cyp B; peptidyl-prolyl isomerase; PPIase; cyclosporin A; CsA; ligand; calcineurin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.8%; Score 44; DB 21; Length 183; 100.0%; Pred. No. 0.33; vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                 Claim 11; Page 1699-1700; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                             disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR32353 standard; Protein; 212 AA.
                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                       99US-0124270.
                                08-MAR-2000; 2000WO-US05988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0740375.
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Best Local Similarity 100...
8; Conservative
                                                                                                                Rosen CA, Ruben SM;
                                                                                                                                    WPI; 2000-587513/55.
N-PSDB; AAF15904.
                                                                                         (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                   183 AA;
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          21-SEP-2000
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Library prepd. from the murine bone marrow derived stromal cell line library prepd. from the murine bone marrow derived stromal cell line ac 6. This cDNA was isolated from a substracted sub-library contg. Genes induced by treatment of the stromal cell line with interleukingens induced by treatment of the stromal cell line with interleuking. I (IL-1). The message levels for cyp C show a 2-3 fold induction by treatment with IL-1, and this cDNA exhibits a high level of homology with known cyclophilins. Cyp C is distinct from mammalian cyclophilins A and B in both sequence and tissue distribution of possesses peptidyl-prolyl isomerase (Pplase) activity which can be completely inhibited by addition of cyclosporin A (CsA). These cyp C fusion proteins can be used as ligands for the identification of intracellular proteins which together form high affinity associations. For example, the cyp C fusion protein binds to a protein of 77 kb in the absence of CsA, while in the presence for CsA it no longer binds to this p77, but instead binds specifically to a protein of 55 kb, identified as calcineurin (U.S.S.N.07/740175).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclophilin-like peptidyl prolyl cis-trans isomerase; CYPB; food processing; Endoplasmic retention signal; cis-trans isomerization; protein secretion; toxin; ADP-glucose pyrophosphorylase; glucanase; beta-1,4-endoglucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                 Cyclophilin C polypeptide and nucleic acid encoding it - useful for screening a tissue-specific immunosuppressive agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.8%; Score 44; DB 14; Length 212;
100.0%; Pred. No. 0.38;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A. niger peptidyl-prolyl cis-trans isomerase (CYPB).
                                                                                                                                                                                       Claim 9; Page 46 + Fig 1; 63pp; English.
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/label= signal_peptide
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Weissman IL;
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990S - 0137222
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990S-0138640
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9905-0132863.
9905-0134218.
9905-0134219.
04-MAY-1999;
05-MAY 1999;
06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
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18-JUN-19
  ö
                                                                                                                 This sequence shows Aspergillus niger cyclophilin-like peptidyl prolyl cis-trans isomerase (CYPB). CYPB is capable of catalyzing the cis-trans isomeration of a peptide bond on the N-terminal side of proline residues in polypeptides. CYPB are useful in methods for increasing the yield of secreted polypeptides from cells. The secreted polypeptides may be enzymes (such as chymocain, thaumatin or alpha-galactosidase) that can be used in food processing, a pest toxin, adenosine diphosphate (ADP)-glucose pyrophosphorylase, a glucanase or beta-1,4-endoglucanase.
                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                               New peptidyl prolyl cis-trans isomerase, designated CYPB, from Aspergillus niger, useful in methods for increasing the yield of secreted polypeptides, such as enzymes used in food processing, from cells
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                                                                                                                                                                                                                           89.8%; Score 44; DB 21; Length 212; 100.0%; Pred. No. 0.38; 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 17119.
                                                                                                   Claim 13; Page 47-48; 52pp; English.
                                                                                                                                                                                                                                                                                                                             AAG16463 standard; Protein; 252 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990S-0121825.
990S-0123180.
990S-0125788.
990S-0125788.
990S-0126785.
990S-0128734.
990S-0128714.
990S-0130077.
990S-0130891.
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                               Conservative
           Derkx PMF, Madrid SM;
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                            WPI; 2000-293167/25.
N-PSDB; AAA08772.
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                   Sequence 212 AA;
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05 - MAR - 1999,
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16 - APR - 1999,
116 - APR - 1999,
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PR 22-JUL-1999; 99US-0145085

PR 22-JUL-1999; 99US-0145087

PR 23-JUL-1999; 99US-0145087

PR 23-JUL-1999; 99US-0145145

PR 23-JUL-1999; 99US-0145145

PR 23-JUL-1999; 99US-0145145

PR 23-JUL-1999; 99US-0145145

PR 23-JUL-1999; 99US-0145218

PR 24-JUL-1999; 99US-0145218

PR 25-JUL-1999; 99US-0145218

PR 25-JUL-1999; 99US-0145313

PR 02-AUG-1999; 99US-0146381

PR 02-AUG-1999; 99US-0146381

PR 02-AUG-1999; 99US-0146381

PR 02-AUG-1999; 99US-0146381

PR 03-AUG-1999; 99US-0146381

PR 04-AUG-1999; 99US-0146381

PR 05-AUG-1999; 99US-0146381

PR 05-AUG-1999; 99US-0146381

PR 11-AUG-1999; 99US-0146381

PR 13-AUG-1999; 99US-0146381

PR 13-AUG-1999; 99US-0146381

PR 13-AUG-1999; 99US-0146381

PR 13-AUG-1999; 99US-0146381

PR 25-AUG-1999; 99US-014931

PR 13-AUG-1999; 99US-014931

PR 27-AUG-1999; 99US-0153130

PR 27-AUG-1999; 99US-015313
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PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160818.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161406.
PR 25-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-
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Search completed: January 15, 2002, 13:05:26 Job time: 197 sec

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	Description	O15729 entamoeba h	09fw22 orvza sativ	043447 homo sapien	Ogcan7 mus musculu	O26994 Foxonlasma	Ogvaha drosophila	Ogd868 mis misculu	001490 orninomyces	O62190 Capporhabdi	O9w227 drosophila	088541 rattus norv	Ogubus taceas more	027716 plasmodium	094190 emericella	Ogbyks homo sanion	Ogdow and Thomas and Ogdow	OAAO2 +aobin long	093826 triaborbite	Ogadio orma catti	ATTAC OT AND OT AND SOUTH
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dР	Ouery Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
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ALIGNMENTS

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Query Match

Length 167; DB 5; Score 50;

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cyclophilin that forms a complex with the U4/U6-specific 60kb and 90kb
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                                                    proteins.";
RNA 4:127-141(1998).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 17, Last annotation update)
01-MILAR TO ARABIDOPSIS THALLANA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
(P34791) (FRAGMENT).
0ryza satia (Rice).
Bukaryota: Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M.,
Chen C.-S., Shaw J.-F.;
"Oryza sariva PAC P0036D10 genomics sequence, complete sequence.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC073405; AAG03106.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=98230239; Pubmed=9570313;
TeigelRamp S., Achsel T., Mundt C., Gothel S.F., Cronshagen U.,
Lane W.S., Marahiel M., Luhrmann R.;
"The 20kD protein of human [04/06.05] tri-snRNPs is a novel
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                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19158 MW; 28EADE80F4625EB9 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
U-SNRNP-ASSOCIATED CYCLOPHILIN (EC 5.2.1.8).
USA-CYP OR CYP-20.
Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                          173 AA.
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                        100.08;
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Best Local Similarity 100.
Matches 9; Conservative
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                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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SEQUENCE 173 AA;
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                              Best Local Similarity
                                                                                                                                                61 DEMIQGEDF 69
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                                                                                                                  1 DFMIQGGDF 9
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                                                       Matches
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043447
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-CSTBL/69; TISSUE-HEAD, EMBRYO, AND CEREBELLUM;

Kawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishil Y.,

Rawai J., Shinaqawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Yamada H.A., Ashburner M., Baralov S., Casavant T.,

RA Saito T., Okazaki Y., Golobori T., Bono H., Rasukawa T., Saito R.,

RA Alsechman W., Gasaterland T., Gissi C., King B., Kochiwa H.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Schriml L., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M., F.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M., R.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Suzuki H., Toyo-Oka K., Wang K.H., Wetlez C., Wilttaker C., Wilming L.,

RA Suzuki H., Toyo-Oka K., Wang K.H., Wetlez C., Whittaker C., Wilming L.,

RA Suzuki H., Toyo-Oka K., Wang K.H., Wetlez C., Wilttaker C., Wilming L.,

RA Winshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                      Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.; "Functional annotation of a full-length mouse CDNA collection."; Nature 409:685-696(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 AA; 19208 MW; 566BCE6361E0F339 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
4833408F11RIK PROTEIN (1100001J08RIK PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; POSO92; ZRMC.
InterPro: IPR002130; CSA_PPIase.
Pfam: PF00160; pro_isomerase; 1.
PRNITS; PR00153; CSAPPISMASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF016371; AAC51927.1; -. EMBL; AF036331; AAC60793.1; -. EMBL; BC003412; AAH03412.1; -.
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Best Local Similarity 100.

Matches 9; Conservative
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TISSUE-CHORIOCARCINOMA;
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us-09-720-469-2.rspt

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1 DFMIQGGDF 9
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Q9V9B9
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High K.P., Joiner K.A., Handschumacher R.E.;
High K.P., Joiner C.A., Handschumacher R.E.;
Biol. Chem. 269:9105-9112(1994).
HEDROTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
HEARLYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
HERTIDE BONDS IN OLIGOPEPTIDES.
HERTIDE REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
HIS BEFECTS VIA AN INHIBITORY ACTION ON PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Álveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
                                                                                                                                                                                                                                                           Gaps
                                   PEPTIDE BONDS IN OLIGOPEPTIDES.

-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
U-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROLYT CIS-TRANS ISOMERASE PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
         FOLDING OF PROTEINS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDYL-PROLYL CIS-TRANS ISOMERASE. DB392502CC0DB6CE CRC64;
                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                               100.0%; Score 50; DB 11; Length 177; 100.0%; Pred. No. 0.037;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 50; DB 5; Length 179; 100.0%; Pred. No. 0.038;
                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                              19208 MW; 566BCE6361E0F339 CRC64;
                                                                                                                                                                                                                                                                                                                                                           179 AA.
                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 18-33.
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                          PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                          EMBL; AK005202; BAB23880.1; -- MGD; MG1:191321; 1100001J08Rik. MGD; MG1:1921150; 4833408F11Rik. InterPro: IPR002130; CSA_PPIBSE.
                                                                                                                                    Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002130; CSA_PPIase.
                                                                   EMBL; AK014665; BAB29493.1; -. EMBL; AK003179; BAB22623.1; -.
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HSSP; P05092; 2CPL.
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                     Isomerase; Rotamase.
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Rest Local Similarity
                                                                                                                                                                                                                                                                                        71 DFMIQGGDF 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Toxoplasma
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Q26994
ID Q2
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RR SEQUENCE FROM N. A.

RADIANSERRELEY;

RA MEDLINE-20196006; PubMed-10731132;

RADIANS-20196006; PubMed-10731132;

RADIANS-20196006; PubMed-10731132;

RADIANS-20196006; PubMed-10731132;

RADIANS-20196006; PubMed-10731132;

RADIANS-20196006; PubMed-10731132;

RADIANS N. Celniker S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J. R., Yandell M. D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfelifer B.D., Hand K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RADIL J.F., Apbayani A., Barendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RADILWAN, Cawley S., Dahke C., Davenport L.B., Davies P.,

Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,

RADIANS B., Delcher A., Deng Z., Mays A.D., Dav I. Dietz S.M.,

RADIANS B., Delcher A., Deng Z., Mays A.D., Dav I.D. Dietz S.M.,

RADIANS B., Delcher A., Deng Z., Mays A.D., Dav I.D. Dietz S.M.,

RADIANS B., Delcher A., Deng Z., Mays A.D., Dav I., Dietz S.M.,

RADIANS B., Delcher A., Deng Z., Mays A.D., Dav I., Dietz S.M.,

RADIANS B., Delcher A., Deng Z., Mays A.D., Dav I., Dietz S.M.,

RADIANS B., Delcher A., Deng Z., Mays A.D., Dav I., Dietz S.M.,

RADIANS B., Mouncell J.H., Gu Z., Gelbart W.M., Relchmin W.,

RADIANS B., Mouncell J.H., Gu Z., Gelbart W.M., Relchmin W.,

RADIANS B., Matter B., Morncoh T.J., Wei M., Nelson D.L.,

RADIANS B., Matter B., Morncoh T.J., Wei M., Nelson D.L.,

RADIANS B., Matter B., Morncoh T.C., Morris J., Moshrefi A.,

RADIANS B., Nelson K.A., Nixon K., Nusskern D. R., Pacleb J.M.,

RADIANS B., Weisenbach J., Ban S., Pollard J., Puri V., Reese M.G.,

Shirskas R., Tector C., Turner R., Venter E., Shen H., Wang Z.-Y., Wang Z.-Y., Wang Z.-Y., Wang Z.-Y., Wang Z.-Y., Wang Sarnman D.A., Weinstenbach J.,

RADIANS B., Weinstenbach J., Weinstenbach J.,

RADIANS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19E5CE187CB9E949 CRC64;
                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                 183 AA.
                                                                                                                                                                                                                                                                                                  Created)
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PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS50072; CSA_PPIASE_2; 1
SEQUENCE 183 AA; 20182 MW; 191
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InterPro, IPR002130; CSA_PPIase.
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                                                                                                                                                                                                        PRELIMINARY;
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73 DFMIQGGDF 81
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Length 183;

Score 50; DB 5; Pred. No. 0.039;

100.0%; 100.0%;

Query Match Best Local Similarity

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Gaps

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0; Indels

Mismatches

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Conservative

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Best Local Similarity
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062190
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                                                                                                                                                                                                                                                                                                                                                                                                                                       C STRAIN-C57BL/G3; TISSUE-SMALL INTESTINE;

RX AGWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kando S., Yamanaka I.,

RA Alzawa K., Jashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsud H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,

RA Korhim L.M., Staubli F., Suzuki R., Tomita M., Maner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Gustinoich S., Hill D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Havashizaki V.
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    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa; Chordata: Cranlata; Vertebrata; Buteleostom!; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID*100909:
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 AA; 20464 MW; E11D29067BA98101 CRC64;
                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2010111B1SRIK PROTEIN.
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    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00160; pro_isomerase: 1.
PROUTS; CAPPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1: 1.
PROSITE: PS50072; CSA_PPIASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AKO08394; BAB25645.1; -. MGD; MGI:1919313; 2010111B15Rik. InterPro; IPR002130; CSA_PPIase.
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Best Local Similarity 100.0%;
Matches 9; Conservative 0.
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    9; Conservative
                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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71 DFMIQGGDF 79
                                                                  77 DFMIQGGDF 85
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                                        1 DFMIQGGDF 9
                                                                                                                                                                                                                                                                                                            2010111B15RIK.
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SEQUENCE
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      Matches
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Q9D868
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MEDLINE-94150718; PubMcd-7906398; Wilson R., Barks M., Wilson R., Anscough R., Anderson K., Barks M., Cooper J., Coulson A., Craxton J., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TEMBLRel. 17, Last annotation update)
PEPTIDIL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(CYCLOPHILIN B) (ROTAMASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam. PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISHRASE.
PROSITE; PS00170; CSA_PPTASE_1; 1.
PROSITE; PS50072; CSA_PPTASE_2; 1.
Isomerase; Rotamase; Signal; Cyclosporin; Endoplasmic reticulum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSA (POTENTIAL).
PREVENT SECRETION FROM ER
SIMILARITY).
A5748C94305B8BE0 CRC64;
                                                                                                                                                                      Eukaryota; Fung1; Chytridiomycota; Neocallimasticales;
Neocallimasticaceae; Orpinomycas.
NCBI_TaxID=50059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AŭG-1998 (TrEMBLrel. 07, Created)
01-AŭG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYP-5 PROTEIN (EC 5.2.1.8).
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.
MEDLINE=95223986; Pubmed=7708690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U17900; AAD04195.1; -. HSSP; P22384; ICYN. Mendel; 20786; URP;1040,20786. Interpro; IPR002130; CSA_PPIASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 AA; 21969 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
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A Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams W.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Adams W.D., Celniker S.E., Hichards S., Ashburner M., Henderson S.N.,
Gocaye R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Bazej R.G., Champe M., Pfeiffer B.D.,
RA Mar K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Baraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Buuck J., Broktetan P., Enttler P.,
RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Rernandez J.R., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbeywam C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Willikinson-Sproat J., Wohldman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota: Neotera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                      -:- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-:- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-:- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-EMBL ISOMERASE FAMILY.
EMBL 729784; CABO7192.1; -.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 AA; 21927 MW; 6216192BFE1FB493 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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                                                                                                                                                                                                                                                                                                                                                     HSSP; P23284; 1CYN.
InterPro; 1PR002130; CSA_PPIase.
Pfam; PP00160; pro; isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                       Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 DFMIQGGDF 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG2852 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (somerase;
                                                                                                                                                                      elegans."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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    g
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A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lash Y., Lia X., Mattei B., McIntosh T.C., McDeod M.P., McPherson D., Mattei B., McIntosh T.C., McDeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Moy M., Murphy B., Murphy L., Murshy D., Nelson D.E., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ralington K., Saunders R.D.C., Scheeler F., Shen H., Spier E., Spradling A.C., Stapleco M., Strong R., Sun E., Spradling A.C., Stapleco M., Strong R., Sun E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X., Wassarman D.A., Weinstook G.M., Weissenbach J., Massarman D.A., Weinstook G.W., Weissenbach J., A., Mang Z.-Y., Wassarman D.A., Weinstook G.W., Weissenbach J., A., Myers E.W., Rubin G.M., Venter J.C., Shu X., Smith H.O., RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., Shu X., Smith H.O., R. The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

C. -- CALLYIC ACTIVITY: CIS-TRANS ISOMERASES ACCELERATE THE C. C. TALLYIT CATIVITY: CIS-TRANS ISOMERASES ACCELERATE THE C. C. TALLYIT CATIVITY: CIS-TRANS ISOMERASES ACCELERATE THE C. C. TALLYIT CATIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC C. PEPDTITE ADALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegiuus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.

EMBL; AE003458; AAF46873.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i FUNCTION: PEPTIDYL-PROINT CISTRANS ISOMERASES ACCELERATE THE POLDING OF PROTEINS (BY SIMILARITY)
-i- CATALYTIC ACTIVITY: CISTRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOREPTIDES.
-i- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.

EMBL, AFO11225, AAC25590.1;
-KSSP: P23284; ICYN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 AA; 22199 MW; A9CEF88B1CC813F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN B (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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STRAIN=WISTAR-KYOTO; TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE BONDS IN OLIGOPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR002130; CSA_PPISSE.
Pfam; PF00160; pro_isomerase: 1.
PROSITE; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P23284; 1CYN.
FlyBase; FBgn0034753; CG2852.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isomerase; Rotamase.
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 DFMIQGGDF 92
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NCBI_TaxID=5072;
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                                                                                                                                                     Reddy G.R.;
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                                                                                                                                                                  ٠;
                                                                                                                                  100.0%; Score 50; DB 11; Length 208; 100.0%; Pred. No. 0.045; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 50; DB 5; Length 210; 100.0%; Pred. No. 0.046; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1999 (TrEMBLrel. 09, Created)
1-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PRECURSOR (EC 5.2.1.8 (ROTANARE) (CYCLOSPILIN) (CYCLOSPORIN A-BINDING PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24049 MW; 778A31CE0FD47D26 CRC64;
                                                                   Isomerase; Rotamase.
SEQUENCE 208 AA; 22802 MW; 02408DFA7157218C CRC64;
                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN.
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                                                                                                                                                                                                                                                                                                                           210 AA.
Pfam, PF00160; pro_isomerase: 1.
PRINTS; PR00153; CSAPPISMRASE
PROSTTE: PS00170; CSA_PPIASE_1: 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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210 AA;
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                                                                                                                                                                                                                           91 DFMIQGGDF 99
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SEQUENCE
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Gaps
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MOI. Biochem. Parasitol. 73:111-122(1995).
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"Aspergillus nidulans cyclophilln B gene (cypB).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PEPTION-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
BEDILNE-94052133; Pubmed-8234327;
Reddy G.R., Chakrabarti D., Schuster S.M., Ferl R.J., Almira E.C.,
Dame J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Emericella nidulans (Aspergillus nidulans).
Eukaryota: Fungi, Ascomycota: Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                 Eukaryota; Alveolata; Apicomplexa; Haemosportda; Plasmodlum.
NCBL_TaxID=36329, 57267, 137071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 210;
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778A359F0FD47D26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN B (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isomerase; Rotamase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 50; DB 5; 100.0%; Pred. No. 0.046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 AA
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Plasmodium falciparum (isolate 3D7),
Plasmodium falciparum (isolate Dd2), and
Plasmodium falciparum (isolate hb3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                 MEDLINE-96123383; PubMed-8577319;
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210 AA;
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Best Local Similarity
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                                                                                                                   SEQUENCE FROM N.A.
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                                    PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
TRANS ISOMERASE FAMILY.

EMBL; AF107254; AAD17998.1; -.
HSSP; P23284; ICYN.
InterPro: PR002130; CSA_PPTASE.
InterPro: PR002130; CSA_PPTASE.
PRINTS; PR0105; CSA_PPTASE.
PROSTIE; PS0015; CSA_PPTASE.;
PROSTIE; PS00170; CSA_PPTASE.;
PROSTIE; PS00170; CSA_PPTASE.;
PROSTIE; PS00170; CSA_PPTASE.;
PROSTIE; PS00014; ER_TARGET; UNKNOWN_1.
-1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9BVK5;
01-JUN-2001 (TTEMBLrel. 17, Created)
01-JUN-2001 (TTEMBLrel. 17, Last sequence update)
01-JUN-2001 (TTEMBLrel. 17, Last annotation update)
01-JUN-2001 (TTEMBLrel. 17, Last annotation update)
PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B).
FURATYCIA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isomerase; Rotamase.
SEQUENCE 214 AA; 23406 MW; 5A4DCFAEBE529DFA CRC64;
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Best Local Similarity 100.
Matches 9; Conservative
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09BVK5
AC 09BVK5, AC 09BVK5, DT 01-JUN-
DT 01-JUN-
DT 01-JUN-
DT 01-JUN-
DC CURALYON
CC MAMMAN 10
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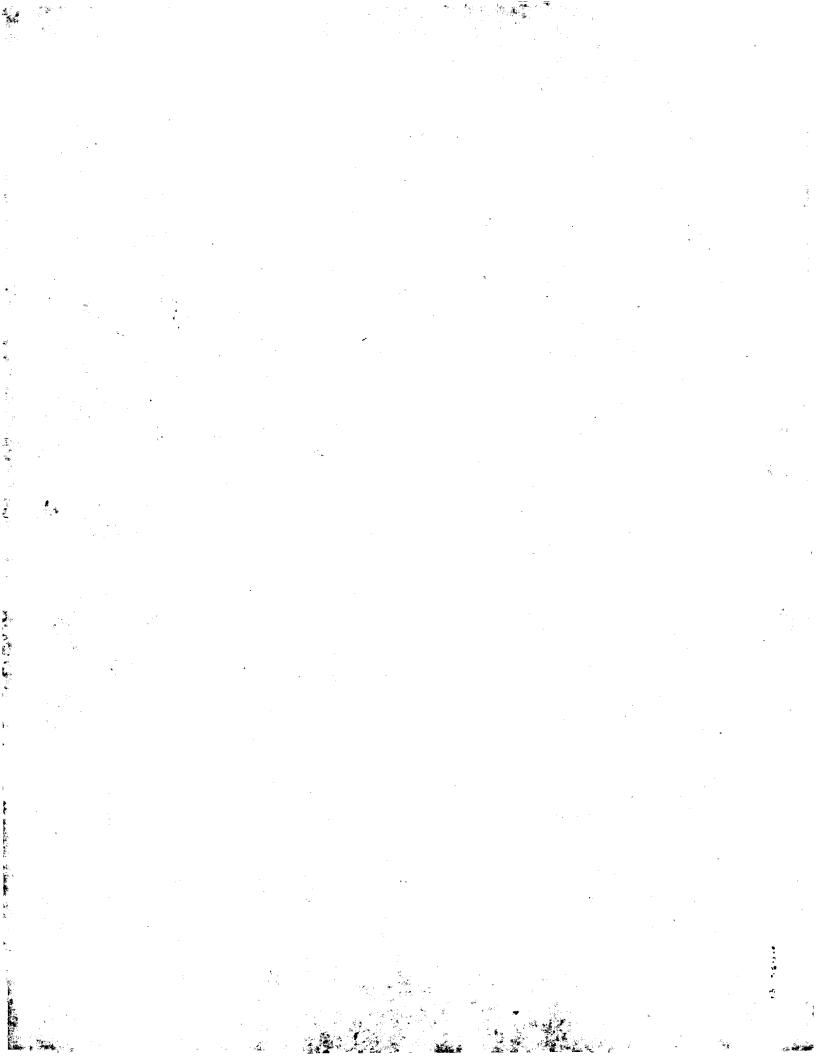
Search completed: January 15, 2002, 13:16:25 Job time: 656 sec

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TYPE: amino acid
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-142-897-5
US-08-142-897-5
US-08-142-897-9
US-08-145-995A-14
US-08-134-852-14
US-08-481-727-14
US-08-481-728A-14
US-08-145-995A-3
US-08-145-995A-3
US-08-145-995A-3
US-09-134-852-4
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US-08-481-747-21
US-08-481-728A-13
US-08-481-728A-13
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US-08-481-738-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-482-728A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212252 seqs, 22503292 residues
                                                                                                                                                                                                                          January 15, 2002, 13:03:58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Match Length
                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
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Maximum DB
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Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 7, M
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Sequence 17, M
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Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 11, Sequence 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/482,728A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: A Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
100.0%; Score 50; DB 2; I
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0;
US-08-142-897-6
US-09-028-366-7
US-09-028-366-7
US-08-451-747-7
US-09-134-852-7
US-08-451-747-15
US-08-451-747-15
US-08-451-747-15
US-08-451-747-15
US-08-451-747-11
US-08-944-604-7
US-08-944-604-7
US-08-944-604-7
US-08-944-604-14
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FILING DATE: 07-UDN-1995
GLESSIFICATION: 435
ATTORREY/AGENT INFORRATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38 304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 781-1969
TELEFAX: (415) 388-3249
TELEX: 910 277299
INFORMATION FOR SEQ 1D NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 amino acids
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      TOPOLOGY: unknown
MOLECULE TYPE: protein
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ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
                     STREET: One Market Pl
CITY: San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                  Sequence 7, Application US/08142897

Sequence No. 5447852

GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy D.
REGISTRATION NUMBER: 34.587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELECHHONE: 415-326-2402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08142897
Patent No. 5447852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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      42 DFMIQGGDF 50
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                                                                                                                                                                                                                                                                                                                                                                                                                               94105
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US-08-142-897-5
                                                                                                           US-08-142-897-7
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESSED: ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: 6 Herbert
ADDRESSEE: 6 Herbert
ATREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/482,728A FILING DATE: UN-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 50; DB 1; Lr
100.0%; Pred. No. 0.077;
                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                                                                                                                                                                                                          PALLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: DUNN, Tracy D.
REGISTRATION NUMBER: 34,587
REPERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
                                                                                                                                                                                                                                                                                                                                                                                                                                   5490A-92-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 16, Application US/08482728A ; Patent No. 5968802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 212 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100...
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-142-897-5
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STATE: California
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Sequence 14. Application US/08145995A

Patent No. 5482850

GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN
                                                              Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 162;
                                                                                                    0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
                                                                DB 1;
                                                              96.0%; Score 48; DB 1
88.9%; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 1
Pred. No. 0.13;
1; Mismatches
                                                                                                      1; Mismatches
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US-08-451-747-14
Sequence 14, Application US/08451747
Sequence 15821107
Batent No. 5821107
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: FESNICK, DAVID S.
REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UF
INFORMATION FOR SEQ 1D NO: 14
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 162 amino acids
                                                          Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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unknown
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-145-995A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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57 DEMLOGGDE 65
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US-08-145-995A-14
      US-08-142-897-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08142897
Patent No. 5447852
GENERAL INFORMATION:
APPLICANT: Welssman, Jeffrey S.
APPLICANT: Welssman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                 Length 126;
                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
      ALLAMALIA RODIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKEY NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELERAX: (415) 781-1989
TELERAX: (415) 789-3249
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                             Score 48; DB 2;
Pred. No. 0.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELECHHONE: 415-326-2402
                                                                                                                                                                                                                                                                                                                                               96.0%;
88.9%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 162 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-482-728A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                 TOPOLOGY: unknown
                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                42 DFMLQGGDF 50
                                                                                                                                                                                                                                                                                                                                                                                                                          1 DFMIQGGDF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-08-142-897-9
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Gaps

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PATION NUMBER: US 08/145,995
FILING DATE: 29-00T-1993
ATTORNEY AGENT INFORMATION:
NAME: RESNICK, DAVID S:
REGISTRATION NUMBER: 34.235
REGISTRATION NUMBER: 43.406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEFAX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                     APPLICATION NUMBER: US/09/134,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 14, Application US/08482728A
; Patent No. 5968802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                           162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.55
"...c 8; Conservative
    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-134-852-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: un}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111:11111
57 DFMLQGGDF 65
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STRET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COMPRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC TITLE OF INVENTION: COMPOUNDS NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC
STREET: 32 TOZER ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09134852
Patent No. 612148
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 162;
0.13;
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                                                                                                                                                                                    ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 2
Pred. No. 0.13;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 96.0
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                      CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-451-747-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 DEMLOGGDE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DFMIQGGDF 9
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APPLICANT: Wang, Bruce
APPLICANT: Payan, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: & Herbert
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPARY: CALILOURIES

ZIP: 94111-4187
COMPUTER READBLE FORM
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OFFRATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: O7-JUN-1995
CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: SILVa ROBIN MARE: 38,304
REGISTRATION NUMBER: 38,304
REGISTRATION NUMBER: 38,304
RECISTRATION NUMBER: 38,304
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION STORY 1989
TELEPROMUNICATION STORY 110 STORY
TELER: 910 277299
INFORMATION FOR SEQ ID NO: 14:
SEQUINCE CHARACTERISTICS:
  DB 3;
Score 48; DB 3;
pred. No. 0.13;
1; Mismatches
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REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELES: 200291 STRE UR
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.08;
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.0
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                    CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DFMIQGGDF 9
                                                                                                                                                                                                                        02109
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                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                           APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                  DB 2; Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 176;
                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREMATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34.235
REGISTRATION NUMBER: 34.235
REGISTRATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEX: 200291 STRE UR
TELEX: 200291 STRE UR
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 1
Pred. No. 0.48;
1; Mismatches
                                                                                                 Score 45; DB
Pred. No. 0.36
1; Mismatches
                                                                                                                                                                                                                                                                              Sequence 3, Application US/08145995A Patent No. 5482850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Sequence 4, Application US/08145995A
; Patent No. 5482850
                                                                                               90.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                          Ouery Match 90.0
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOSTON
: MASSACHUSETTS
: USA
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 90.0
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS: single
unknown
          TOPOLOGY: unknown

MOLECULE TYPE: protein
US-08-482-728A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                          1 DFMIQGGDF 9
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50 NFMIQGGDF 58
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                            RESULT 10
US-08-145-995A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-08-145-995A-4
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Petent No. 5821107

GENERAL INFORMATION:

APPLICANT: PAGE, ANTONY

TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC

TITLE OF INVENTION: COMPOUNDS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.

STREET: 32 TOZER ROAD

CITY: BEVERLY

STATE: MASSACHUSETTS

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
GENERAL INFORMATION:

APPLICANT: CARLOW, CLOTILDE K.S.

APPLICANT: PAGE, ANTONY
TILLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 01915

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 1;
Pred. No. 0.48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/145,995A FILING DATE: 29-OCT-1993 CLASSIFICATION: 435 ATTONNEY/AGENT INFORMATION: NAME: REGISTRATION NUMBER: 34235
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Gaps
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Sequence 3, Application US/09134852

Patent No. 6127148

GENERAL INFORMATION:

APPLICANT: CARLOW, CLOTILDE K.S.

APPLICANT: PAGE, ANTONY

TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC

TITLE OF INVENTION: COMPOUNDS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: DAVID G. CONLIN: DIKE, BRONSTEIN, ROBERTS 6

ADDRESSEE: CUSHMAN

STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 176;
                                                                                                                                                                                   Score 45; DB 2; Length 176;
Pred. No. 0.48;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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APPLICATION NUMBER: US/09/134,852
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 3;
Pred, No. 0.48;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DUMBER:
FILING DATE: 29-CCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REFERENCE/DOCKET NUMBER: 43406
TELEPHONE: (617) 523-3400
TELEPHONE: (617) 623-3400
TELEPHONE: (617) 623-3640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.08;
                                                                                                                                                                                            90.0%;
88.9%;
                 LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                          Query Match 90.0
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-09-134-852-3
                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :||||||||
70 NFMIQGGDF 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-134-852-3
                                                                                                                             US-08-451-747-4
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US-08451-747-4

Sequence 4, Application US/08451747

Patent No. 5821107

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: WETHOD FOR IDENTIFYING ANTI-PARASITIC

TITLE OF INVENTION: COMPOUNDS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSE: ADDRESSE:

CITY: BEVERT:

STREET: 32 TOZER ROAD

CITY: BEVERLY

STATE: MASSACHUSETIS

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZOUNTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 2;
Pred. No. 0.48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: 30901
TELECOMMUNICATION INFORMATION:
                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMMUNICATION INFORMATION:
TELEFRAM: (508) 927-5054
TELEFAX: (508) 927-1705
      APPLICATION NUMBER: US/08/451,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
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88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 8; Conserv
                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DFMIQGGDF 9
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RESULT 15

15 Sequence 4, Application US/09134852

15 Sequence 4, Application US/09134852

16 REMEAL INFORMATION:

17 PAPLICANT: RAGE ANYOW

17 TILE OF INVENTION: WETHOD FOR IDENTIFYING ANTI-PARASITIC

17 TILE OF INVENTION: COMPOUNDS

18 OF ADDRESSEE: COURTERS:

18 ADDRESSEE: CUSHAMA

18 OF ADDRESSEE: CUSHAMA

19 OF ADDRESSEE: CUSHAMA

19 OF ADDRESSEE: CUSHAMA

19 OF ADDRESSEE: CUSHAMA

19 OF ADDRESSEE: COUNTRY: USA

19 OF ADDRESSEE: COUNTRY: USA

27 TITE OF INVENTION: COMPOUNDS

19 OF ADDRESSEE: COUNTRY: USA

27 TITE OF INVENTION: COMPOUNDS

19 OF ADDRESSEE: COUNTRY: USA

27 TITE OF INVENTION: COUNTRY: USA

28 OF TALLCATION UNHBER: US/09/134,852

29 OF TITE OF OF TALLCATION UNHBER: US/09/145,995

37 TITE OF ADDRESSEE: OF OF OF TELEPAX: (617) 523-340

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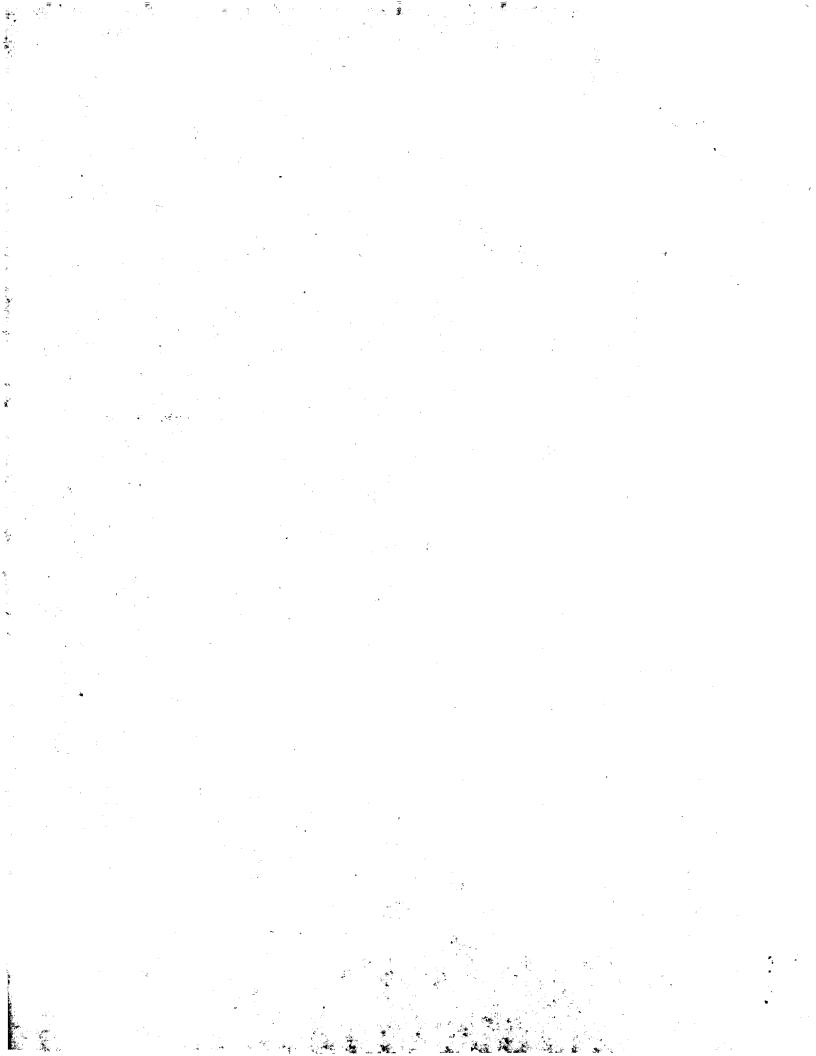
TELEPAX: (617) 523-340

TELEPAX: (617) 523-34
```

; 0 ö 90.0%; Score 45; DB 3; Length 176; 88.9%; Pred. No. 0.48; Live 1; Mismatches 0; Indels 0; Indels Query Match
Best Local Similarity 88.9
Matches 8; Conservative

1 DFMIQGGDF 9 :11111111 70 NFMIQGGDF 78

Search completed: January 15, 2002, 13:03:58 Job time: 214 sec



us-09-720-469-2.rsp

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 15, 2002, 13:14:58 ; Search time 24.88 Seconds (Without alignments) 13.263 Million cell updates/sec Run on:

US-09-720-469-2 50 1 DAMIQGCDF)9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

iptio	O00066 fa			-			P24369 mus musculu		P30412 mus musculu	P34791 arabidopsis		-	-	P52015 caenorhabdi	P52009 caenorhabdi	P52011 caenorhabdi	P52014 caenorhabdi		Q41651 vicia faba	Q27450 brugia mala		P30414 homo sapien	P25719 saccharomyc	P23285 saccharomyc	P45877 homo sapien	O66105 treponema p	P10255 neurospora	P26882 bos taurus	Q08752 homo sapien	_	P18253 schizosacch	295	P21569 zea mays (m
SUMMARIES	CYPH_UROFA	CYPB_CAEEL	CYP5_CAEEL	CYPB_CHICK	CYPB_BOVIN	CYPB_HUMAN	CYPB_MOUSE	CYPB_RAT	CYPC_MOUSE	CYP4_ARATH	CYPH_YEAST	PPI_STRCH	CYP2_CAEEL	CYP7_CAEEL	CYP1_CAEEL	CYP3_CAEEL	CYP6_CAEEL	CYPD_YEAST	CYPB_VICFA	CYP1_BRUMA	NKCR_MOUSE	NKCR_HUMAN	CYPC_YEAST	CYPB_YEAST	CYPC_HUMAN	PPIB_TREPA	CYPH_NEUCR	CYP4_BOVIN	CYP4_HUMAN	CYPH_CANAL	CYPH_SCHPO	CYP2_ARATH	CYPH_MAIZE
Length DB	163 1	183 1			208 1			208 1	212 1	260 1	161	165 1	171 1	1/1	192 1	173 1	707	225 1	248 I	843 1	1453 1	1462 1	187	7 CO2		712			370 1			169 1	1/2 1
% Query Match L	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	0.0	96.0	0.0	92.0	92.0	0.0	90.0	90.0	90.0	90.0	90.0	0.0	0.0	0.00	0.00	0.88	0.00	0.88	0.88	84.0	84.0	84.0	82.0
Score	50	20	50	20	20	20	0 1	0,0	000	00	æ •	2.4	4	9 .	.	4 -	4. •		4. V	45	4 U r	φ·	4.						4.0	24.	24.	2 .	4
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Gaps

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Query Match 100.0%; Score 50; DB 1; Length 163; Best Local Similarity 100.0%; Pred. No. 0.0064; Matches 9; Conservative 0; Mismatches 0; Indels

1 DFMIQGGDF 9

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09v3g3 drosophila P87051 schizosacch P8485 blattella g P25007 drosophila P34790 arabidopsis O49886 lupinus lut P34887 allium cepa P14088 echinococcu P64374 bos taurus P14851 cricetulus P17742 mus musculu P17712 mus musculu P10111 rattus norv
CYPE DROWE CYPZ_SCHPO CYPH_BLAGE CYPH_DROWE CYPH_LUPLU CYPH_LUPLU CYPH_LUPLU CYPH_LOE CYPH_ALLCE CYPH_BOXIN CYPH_BOXIN CYPH_ECHGR CYPH_ROUSE CYPH_MOUSE
пенининання
300 155 165 172 172 172 163 163 163
880.0 880.0 880.0 880.0 78.0 78.0 78.0
444444888888 HOOOOOOOOOO

ALIGNMENTS

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PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 5 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
             (CYCLOPHILIN-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYPB_CHICK P24367:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                          Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                       Page A.P., Macniven K., Hengartner M.O.;
Cloning and blochemical characterization of the cyclophilin
homologues from the free-living nematode Caenorhabditis elegans.";
Blochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-i- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 11 (EC 5.2.1.8) (PPIASE)
CYP-11 OR T01B7.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 183;
                                                                                                                                                                                                                                                                                                                                          Sims M.; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moterpro; 19802130; CSA_PPISSE.

Pfam; PF00160; pro_isomerase; 1.

PRINTS; PR00151; CSA_PPISNRASE.

PROSITE; PS00170; CSA_PPIASE_1; 1.

PROSITE; PS0072; CSA_PPIASE_2; 1.

PROSITE; Rotanase; Multigene family.

SEQUENCE 183 AA; 20193 MW; 23549C922828C533 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 50; DB 1; L
100.0%; Pred. No. 0.0072;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 35, Last annotation update)
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                                                                      183 AA.
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                                                                                                                                                                                                                                               MEDLINE=96276416; PubMed=8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U34955; AAC47115.1; -. EMBL; Z66499; CAA91297.1; -. HSSP; P05092; 3CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WormPep; T01B7.4; CE03588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                       STANDARD;
                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 DFMIQGGDF 85
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
               65
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                                                                                                                                                                                                 NCBI_TaxID=6239;
   11111111
57 DFMIQGGDF
                                                                                                                                                                                                                                      STRAIN-BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996
01-OCT-1996
01-NOV-1997
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P52013;
                                                                        CYPB_CAEEL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
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15-JUL-1999 (Rel. 38, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
MEDLINE-91250364; PubMed-2040593;
Caroni P., Rothenfluh A., McGlynn E., Schneider C.;
Caroni P., Rothenfluh A., McGlynn E., Schneider C.;
"S-cyclophilin. New member of the cyclophilin family associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-96276416; PubMed-8694762;
Page A.P. Macniven K., Hengartner M.O.;
Page A.P. Macniven K., Hengartner M.O.;
"Cloning and biochemical characterization of the cyclophilln homologues from the free-living nematode Caenorhabditis elegans.";
Biochem. J. 317:179-185(1996).
-i. FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-i. FUNCTION: DPIASES ACCELERATE THE FOLDING OF PROLINE IMIDIC PERTIDE BONDS IN OLICOPEPTIDES.
-i. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the secretory pathway.";
Lib secretory pathway.";
Lib sholl chem. 266:10739-10742(1991).
Lib sholl chem. 266:10739-10742(1991).
Lib sholl prints accelerate the Folding of Proline Imidic
Lib caralytic activity: cis-trans isomerization of Proline Imidic
Peptide Bonds in OligoPeptides.
Lib enzyme regulation: CYCLOSPORIN A (CSA) INHIBITS GYPB.
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Pfam; PF00160; pro_isomerase; 1.
PRONO153; CSAPPISWRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS0072; CSA_PPIASE_2; 1.
Isomerase; Rotamase; Multiqene family.
ESQUENCE 204 AA; 22366 WW; 22ABB39AD1127BAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 AA.
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Caenorhabditis elegans.
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Best Local Similarity
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208 AA;
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Matches 9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multigene family.
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                                                                                                                                                                                                                                                                                                                HSSP; P23284;
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P23284;
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CYPB_HUMAN
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SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY). SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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01-JUN-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
EPPTIOYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
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Galat A., Bouet F.;
"Cyclophilin-B is an abundant protein whose conformation is similar
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Sukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovinae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PREVENT SECRETION FROM ER
                                                                                                                                                                                                                                                                                                                                                                               Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carrello A., Mark P.J., House A.K., Ratajczak T.;
Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NY SIMILARITY).
D9C0C2E528E25B59 CRC64;
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HSSP, P22384; 1CXN.
Interpro; IPR002130; CSA_PPIase.
Pfam; PP00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMSAS.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS500772; CSA_PPIASE_2; 1.
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FEBS Lett. 347:31-36(1994).
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Matches 9; Conservative
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P80311;
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ID CYPB_BOVIN
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01-NOV-1991 (Rel. 20, Last sequence update)
20-ANG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
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Proc. Natl. Acad. Sci. U.S.A. 88:1903-1907(1991).
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CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
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Usukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
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                                                        ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB. SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 50; DB 1; Length 208; 100.0%; Pred. No. 0.0083; Pred. 0; Mismatches 0; Indels
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0097C88289AF6276 CRC64;
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MEDLINE-91260697; PubMed-1710767;
Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.,
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MEDLINE-91156714; PubMed-2000394;
                            PEPTIDE BONDS IN OLIGOPEPTIDES.
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Pfam: PF00160; pro_isomerase; 1.
PRINTS: PR00153; CSAPPIBMRASE.
PROSITE; PS00170; CSA_PPIASE_1; IPROSITE; PS50072; CSA_PPIASE_2; 1.
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208 PF
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22701 MW;
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208 AA
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Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
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EMBL; X58990; CAA41736.1; -.
PIR; 393722; B33722.
PIR; S21835; S21835.
HSSP; P23284; 1CYN.
MGD; MGI:97750; Pplb.
                                                             01-MAR-1992 (Rel. 21, Created)
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احد 9; Conservative
   STANDARD;
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SEQUENCE FROM N.A.
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CYPB_MOUSE
P24369;
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                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION.
MEDLINE-92112948; PubMed-1530944;
Arber S., Krause K.-H., Caroni P.;
"S-cyclophilin is retained intracellularly via a unique COOH-terminal sequence and colocalizes with the calcium storage protein calreticulin.";
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Mikol V., Kallen J., Walkinshaw M.D.;
*X-ray structure of a cyclophilin B/cyclosporin complex: comparison
with cyclophilin A and delineation of its calcineurin-binding
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208 PREVENT SECRETION FROM ER.
22742 MW; A814481B7EBD4579 CRC64;
                                                                                                                                                                                                                     "Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 91:5183-5186(1994).
-!- FUNCTION: PIPASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- ENZYME REGLEMATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULM LUMEN.
-!- SUMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS0072; CSA_PPIASE_2; 1.
Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
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   endoplasmic reticulum-specific cyclophilin."; Cell. Biol. 11:3484-3491(1991).
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EMBL; M63573; AAA36601.1; ALT_INIT.
EMBL; M60457; AAA35733.1; --
PIR; A39118; CSMUB.
PIR; A40515; A40515.
PDB; ICXN; 29-JAN-96.
                                                                                             SEQUENCE OF 64-76 AND 151-157.
MEDLINE-93162043; PubMed-1286667;
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208 AA;
                                                                                                                                                                                           Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DFMIQGGDF 9
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SIGNAL

RESULT 7 CYPB_MOUSE

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01-WAR-1992 (Rel. 21, Last sequence update)
15-U01-1999 (Rel. 38, Last annotation update)
PEPTIDYL-PROLY CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
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4BBDF5AE40BAD3A7 CRC64;
                                                                                                                                                                                                                                                                                     MEDLINE-91260697; PubMed-1710767;
Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;
"An endoplasmic reticulum-specific cyclophilin.";
Mol. Cell. Biol. 11:3484-3491(1991).
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01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                        REVISIONS TO C-TERMINUS.
MEDLINE-92112948; Pubmed-1530944;
Arber S., Krause K.-H., Caroni P.;
"S-cyclophilin is retained intracellularly via a unique COOH-terminal
                                                                                   Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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76D12AC3427FEF32 CRC64;
                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-90300692; PubMed=2194066;
Iwai N., Inagami T.;
"Molecular cloning of a complementary DNA to rat cyclophilin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                        Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 50; DB 1; Length 208; 100.0%; Pred. No. 0.0083;
                                                                                                                                                                                                                                                     sequence and colocalizes with the calcium storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR002130; CSA_PPIBSE.
Pfam; PF00160; pro_isomerase; 1.
PRNUTS; PR00153; CSAPPISKRSE.
PROSITE; PS00170; CSA_PFIASE_1; 1.
PROSITE; PS50072; CSA_PFIASE_2; 1.
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MEDLINE-91347379; PubMed=1652374;
                                                                                                                                                                          protein mRNA,";
Kidney Int. 37:1460-1465(1990).
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Matches 9; Conservative
                                                                           Rattus norvegicus (Rat).
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208
208
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                                                                                                           NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Multigene family.
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                                                                                                                                                                                                                                                                 calreticulin.
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CYPC_MOUSE
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01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR
(EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Jman J., Weissman I.L.; cytoplasmic candidates for immunophilin action are revealed by cytoplasmic candidates for immunophilin action are revealed by bity for a new cyclophilin; one in the
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                                                      absence of CSA.";
c1-16116:1799-806(1991).
c1-1 FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
c1-1 CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PETTIDE BONDS IN OLIGOPEPTIDES.
c1-1 ENZYME REGULATION: CYCLOSPORINA (CSA) INHIBITS CYPC.
c1-1 SUBCELLULAR LOCATION: CYTOPLASMIC.
c1-2 SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and characterization of chloroplast and cytosolic forms cyclophilin from Arabidopsis thaliana.";
J. Biol. Chem. 269:7863-7868(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. COLUMBIA;
MEDLINE-98088013; PubMed=9426607;
Chou I.T., Gasser C.S.;
"Characterization of the cyclophilin gene family of Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lippuner V., Chou I.T., Scott S.V., Ettinger W.F., Theg S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 212;
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SEQUENCE 212 AA; 22794 MW; C99E7AA5D0FA04B6 CRC64;
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Pred. No. 0.0085;
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InterPro: IPR002130; CSA_PPIase.
Pfan; PP00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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MEDLINE=94179146; Pubmed=8132503;
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100.0%;
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Best Local Similarity
Matches 9; Conserv
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                                                                                       SEQUENCE FROM N.A.

C STRAIN—CV. COLUMBIA;
Choisne N., Robert C., Brottier P., Wincker P., Cattolico L.,
Choisne N., Robert C., Brottier P., Wincker P., Cattolico L.,
Choisne N., Robert C., Brottier P., Weissenbach J., Mewes H.-W., Lemcke K.,
A Artiquenave F., Saurin W., Weissenbach J., Mewes H.-W., Lemcke K.,
A Mayer K.F.X., Quetier F., Salanoubat M.;
LS SUBMILIER (FEB-2000) to the EMBL/GenBank/DDBJ databases.
LS CHONCTION: PPIASES ACCELERATE THE FOLDING OF PROLINE IMIDIC
C PRETIDE BONNES IN OLIGOPEPTIDES.
C -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
C PRETIDE BONNES IN OLIGOPEPTIDES.
C -1- ENZYME REGULATION: BINDS CYCLOSORIN A (CSA). CSA MEDIATES SOME
C -1- SUBCELLULAR LOCATION: CHLOROPLAST STROMA.
C -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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01-FB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYCLOPHILIN (CYCLOSPORIN A-BINDING PROTEIN) (CPH) (PPI-II).
CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) (CPH) (PPI-II).
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungl: Agcomycota: Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dietmeier K., Tropschug M.;
"Nucleotide sequence of a full-length cDNA coding for cyclophilin
(peptidy)-prolyl cis-trans isomerase) of Saccharomyces cerevisiae.";
Nucleic Acids Res. 18:373-373(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
thaliana and phylogenetic analysis of known cyclophilin proteins.";
Piant Mol. Biol. 35:873-892(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHLOROPLAST (POTENTIAL).
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
D412AECBB8A5A3B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P23284; ICYN.
SWISS-2DPAGE; P34791; ARATH.
InterPro; IPR002130; CSAPITASe.
Pfam: PF00160; pro_lsomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1: 1.
PROSITE; PS00170; CSA_PPIASE_2: 1.
Cyclosporin; Isomerase; Rotamase; Chloroplast; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90221831; PubMed-2183184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U42724; AAB96831.1; -. AL138642; CAB71910.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 260 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L14845; AAA20048.1; -.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 DFMIQGGDF 158
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CYPHY
AC P14832
DT 01-APR
DT 01-FBB
DT 15-DEC
DE PEPTID
DE PEPTID
DE CYCLO
GN CPRI 0
GN CPRI 1
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01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
CYCLOPHILIN HOWOLOG).
Streptomyces chrysomallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Purification and properties of multiple molecular forms of yeast peptification and properties of multiple molecular forms of yeast peptification and properties of multiple molecular forms of yeast peptification and properties of multiple molecular forms of yeast benchim. Blophys. Acta L161:161-167 (1993).

-!- RUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
-!- SUBCELULIAR LOCATION: CYTOPIASMIC.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                             "Yeast cyclophilin: isolation and characterization of the protein,
                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
STRAIN-S288C / AB972;
Murphy L., Richards C., Harris D., Barrell B.G., Rajandream M.A.,
Walsh S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclosporin; Isomerase; Rotamase; Multigene family; Acetylation.
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90076969; PubMed-2687115;
Haendler B., Keller R., Hiestand P.C., Kocher H.P., Wegmann G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLATION.
CE2B71DB8D8C44D7 CRC64;
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Pred. No. 0.016;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION, AND PARTIAL SEQUENCE.
MEDLINE-93160233; PubMed-8431466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGD; SO002562; CPH1.
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_Isomerase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 AA; 17259 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X17505; CAA35545.1; -. EMBL; M30513; AAA34528.1; -. EMBL; Z50046; CAA90376.1; -.
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S25443; CSBY.
PIR; S29645; S29645.
                                                                                                                                                                                         Gene 83:39-46(1989).
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56 DFMLQGGDF 64
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                                                                                                                                                                     gene
                                                                                                   Movva N.R.;
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Q06118;
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SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYP7_CAEEL
P52015;
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                                                                                                                                                                                                                                                                                                                                                                       Matches
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01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 2 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                       Pahl A., Ushlein M., Bang H., Schlumbohm W., Keller U.;
"Streptomycetes possess peptidy1-proly1 cis-trans isomerases that
strongly resemble cyclophilins from eukaryotic organisms.";
Mol. Microbiol. 6:351-358(1992)
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMBRIZATION OF PROLINE IMDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
-!- SUBCELLULAR LOCATION: CYTOPHASMIC.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page A.P., Macriven K., Hengartner M.O., "Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans."; Biochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.0%; Score 48; DB 1; Length 165; 88.9%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n; Isomerase; Rotamase.
165 AA; 17716 MW; 2CFIDF725CD6F47D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.01
1; Mismatches
                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 4-41.
                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                             STRAIN-ATCC 11523;
MEDLINE-93116593; PubMed-1474897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
MEDLINE-96276416; Pubmed-8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P05092; 3CYS.
InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 215137; CAA78840.1; -. PIR; S28020; S28020.
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Best Local Similarity 88.5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111:1111
58 DFMLQGGDF 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DFMIQGGDF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyclosporin;
SEQUENCE 16
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P52010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P2_CAEEL
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20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLIT CIS-TRANS ISOMERASE 7 (EC 5.2.1.8) (PPIASE) (ROTAWASE)
CYCLOPHILIN-7).
CYP-7 OR Y75B12B.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-13.
STRAIN-BRISTOL N2;
MEDLINE-97295299; PubMed-9150941;
Bini L., Heid H., Liberatori S., Geier G., Pallini V., Zwilling R.;
"Two-dimensional gel electrophoresis of Caenorhabditis elegans homogenates and identification of protein spots by microsequencing.";
Electrophoresis 18:557-562(1997).
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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*Cloning and biochemical characterization of the cyclophilin
homologues from the free-living nematode Caenorhabditis elegans.";
Biochem. J. 317:179-185(1996).
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-i- CATALYTIC ACTULTY: CISTRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-i- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 171;
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                                                                                                                                                                                                                                                                                                                                Isomerase; Rotamase; Multigene family.
SEQUENCE 171 AA; 18416 MW; 23498E7AA437034C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 1;
Pred. No. 0.041;
1; Mismatches
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InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; Pro_isomerase; 1.
PRINTS: PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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                                                                                                                                                                             EMBL; U34354; AAC47127.1; -.
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88.9%;
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Best Local Similarity
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EFMIQGGDF 74
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page A.P., Macniven K., Hengartner M.O.; "Cloning and blochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans."; Blochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                                                                                       EMBL, U27559; AAC47125.1; -.

R EMBL, U27559; AAC47125.1; -.

R HSSP, P05092; 1AWV.

R WOTMPEP; Y75B12B.2; CE20371.

R MOTMPEP; Y75B12B.2; CE20371.

R MOTMPEP; PR00153; CSA_PPIASE.

R PRINTS; PR00153; CSA_PPIASE.

R PROSITE; PS00170; CSA_PPIASE.1; 1.

R PROSITE; PS50072; CSA_PPIASE.2; 1.

RW ISOGNERASE; RCLAMBASE, Multigene family.

FT CONFLICT 12 12 1 -> T (IN REF. 1).
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MEDLINE-96276416; PubMed-8694762;
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EMBL; AL033512; CAA22075.1;
HSSP; P05092; 1AWV.
WormPep; Y49A3A.5; CE22213.
InterPro; IPR002130; CSA_PPIBSE.
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                        Length 192;
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1: 1.
PROSITE; PS00170; CSA_PPIASE_2: 1.
PROSITE; PS00170; CSA_PPIASE_2: 1.
PROGITE; PS00170; CSA_PPIASE_2: 1.
PSOMERASE; Rotanase; Multigene family.
SEQUENCE: 192 AA; 20710 MW; C2094D91809ECE85 CRC64;
                                                                                                                                                                        Score 46; DB 1;
Pred. No. 0.047;
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                                                                                                                                                                        92.0%;
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Best Local Similarity 88.9
Matches 8; Conservative
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84 EFMIQGGDF
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 15, 2002, 13:06:15; Search time 42.04 Seconds (without alignments) 16.308 Million cell updates/sec

US-09-720-469-2 50 1 DFMIQGGDF 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	peptidylprolyl iso	, ,				peptidylprolyl iso			peptidylprolyl iso	CDC28/cdc2-like ki		_			peptidylprolyl iso		_	_	_	_	_	ч	killer	lprolvl		peptidylprolyl iso				1
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\$12324 A54204 A71261 A71261 CSNCM S71849 T49204 A46579 A45879 E86736 F84808 F84808 CSCZPA CSZPA T50838	T31517
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ALIGNMENTS

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rase (EC 5.2.1.8) [similarity] - Toxoplasma gondii ha gondii #sequence_revision 06-Jan-1995 #text_change 08-Sep-2000 ', K.A.; Handschumacher, R.E. 9105-9112, 1994 cDNA sequences, and biochemical characterization of the major cyc A53522; MUID:94179329						A;Experimental source: liver G;Superfamily: peptidylprolyl isomerase: cyclophillin homology C;Reywords: cis-trans-isomerase C;Reywords: cis-trans-isomerase F;1-183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental <mat> F;10-172/Domain: cyclophilin homology <cyp></cyp></mat>
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 Toxoplasma gondii #text_change 08-Sep characterization o 	ушо	Len		rext.	arfke 199	home J.3K
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arit; n-19° R.E.	loph	0 9		3К -	J.; S	lophi
imila 5-Jan er, 1 5jocl	cyc.	50; No. Natel		20.3K	d, t	cyc]
A53522 peptidylprolyl isomerase (EC 5.2.1.8) [similarity] - Toxoplasma gondii N;Contains: cyclophilin C;Species: Toxoplasma gondii C;Species: Toxoplasma gondii C;Species: Toxoplasma gondii C;Bate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-2000 C;Accession: A53522 R;H19h, K.P.; Joiner, K.A.; Handschumacher, R.E. R;H19h, K.P.; Joiner, K.A.; Handschumacher, R.E. A; Biol. Chem. 269, 9105-9112, 1994 A;Title: Isolation, cDNA sequences, and biochemical characterization of the A;Reference number: A53522; MUID:94179329 A;Accession: A53522	A;Wolecule type: mRNA A;Residues: 1-179 <higa A;Cross-references: GB:U04633 C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase F;22-178/Domain: cyclophilin homology <cyp></cyp></higa 	Score 50; D Pred. No. 0. Mismatches		RESULT 2 S71547 peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat N;Alternate names: cyclophilin B; PPIASE C:Species: Rattus norvegicus (Norway rat) C;Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999 C;Accession: S71547	R;Ruecknagel, K.P.; Pfeifer, T.; Rahfeld, J.U.; Schaerfke, submitted to the Protein Sequence Database, November 1996 A;Reference number: S71547 A;Accession: S71547 A;Molecule type: protein A;Residues: 1.183 a KUES.	A.Experimental source: liver C.Superfamily: peptidylprolyl isomerase; cyclophilin homology C.Keywords: cis-trans-isomerase F.1-183/Product: peptidylprolyl isomerase, isoform 20.3K #sta F.1-172/Domain: cyclophilin homology <cyp></cyp>
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roly roly .: To 5-Jai .p.; .P.; .them .sola .ce nu	styl s: 1 seferentily nily s: c:	atch	DFM DFM	2 roly] te në : Rat 5-Nov	yel, to to to to to to to to	ental
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change OB-Sep-2000
C;Accession: T18578; T24269
R; Page, A. P.; MacNiven, K.
submitted to the EMBL Data Library, August 1995
A; Reference number: 218986
A; Accession: T18578
A; Accession: T18578
A; Accession: T18578
A; Accession: T18578
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Reference number: 21867
A; Cross-references: EMBL:034955; PIDN:AAC47115.1
A; Experimental source: strain Bristol N2
B; Sins, M.
submitted to the EMBL Data Library, October 1995
A; Reference number: 21867
A; Accession: T74269
A; Reference number: 21867
A; Accession: T4269
A; Residues: 1-183 <WILL>
A; Experimental source: clone T0187
C; Genetics:
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A; Man pos
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aubmitted to the EMBL Data Library, March 1997
A;Reference number: 219446
A;Reference number: 219446
A;Accession: T21587
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A;Molecule type: DNA
A;Residues: 1-204 <MIL>
A;Residues: 1-204 <MIL>
A;Residues: 1-204 <MIL>
A;Cossereferences: EMBL:292784; PIDN:CAB07192.1; GSPDB:GN00019; CESP:F31C3.1
A;Experimental source: Clone F31C3
C;Genetics:
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Pred. No. 0.0065;
Mismatches 0; Indels
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A;Introns: 34/3; 87/3; 148/1
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase
F;16-183/Domain: cyclophilin homology <CYP>
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   Indels
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0
   Mismatches
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ő
                                                                                                                                                                                                                                                                                                                                                    N;Contains: cyclophilin
C;Species: Caenorhabditis elegans
   9; Conservative
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                                                                                                                                    66 DFMIQGGDF 74
                                                                    1 DFMIQGGDF 9
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   Matches
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A,Molecule type: mRNA A;Residues: 'MLRLSERN',1-208 <SPI> A;Cross-references: GB:M63573; NID:q337998; PIDN:AAA36601.1; PID:g337999 A;Cross-references: GB:M63573; NID:g337998; PIDN:AAA36601.1; PID:g337999 A;Cross-teferences: GB:M63573; NID:g337998; PIDN:AAA36601.1; PID:g337999 A;Cross-teferences: Call this sequence, including the amino end of the mature form, were conf A;Note: parts of this sequence, including the amino end of the mature form, were conf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptidylprolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken C; Species: Gallus gallus (chicken) C; Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999 C; Accession: A40516 Feb-1992 #sequence_revision 28-Feb-1992 #sequence_revision 28-Feb-1992 #sequence_revision 28-Feb-1992 #sequence_revision 8. A0516 Feb-1992 #sequence_revision Figure 1992 Feb-1993 #sequence 1993 #sequence 1993 #sequence 1993 #sequence 1993 #sequence number: A5016 #sequence number: A40516 #sequence number: A40516 #sequence number: A50516 
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C; Date: 31-Mar.1992 #text_change 08-Dec-2000
C; Date: 31-Mar.1992 #sequence_revision 31-Mar.1992 #text_change 08-Dec-2000
C; Accession: A39118; A39722; A40515; S65742
F; Price, E.R.; Zydowsky, L.D.; Jin, M.; Bakcr, C.H.; McKeon, F.D.; Walsh, C.T.
Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991
A; Title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl iso A; Accession: A39118; MUID:91156714
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A; Residues: 1-208 <+HAS>
A; Pibli Chem. 266, 10735-10738, 1991
A; Tibli Chem. 266, 10735-10738, 1991
A; Tible: A novel secreted cyclophilin-like protein (SCYLP).
A; Reference number: A40515; MUID:91250363
A; Accession: A40515
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A; Residues: 1-208 <PRI>
A; Cross-references: GB:M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335
A; Hasel, K. W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
Mol. Cell. Biol. 11, 3484-3491, 1991
A; Title: An endoplasmic reticulum-specific cyclophilin.
A; Reference number: A39722; MUID:91260697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNÁ
A; Residues: 1-207 < CAR>
A; Cross-references: GB: M63553; NID:g212648; PIDN:AAA49064.1; PID:g212649
A; Cross-references: GB: M63553; NID:g212648; PIDN:AAA49064.1; PID:g212649
C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
C; Keywords: cis-trans-isomerase; cyclosporin A binding
F; 34-196/Domain: cyclophilin homology < CYP>
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             Length
Score 50; DB 2; I
Pred. No. 0.0073;
; Mismatches 0;
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Conservative
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A; Accession: S21835
A; Status: preliminary
                                                                                    A; Molecule type: mRNA
A; Residues: 1-216 <SCH>
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A; Residues: 9-216 <NOR>
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Best Local Similarity
Matches 9; Conserv
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                                                                A;Status: preliminary
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                                   A; Accession: A56861
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R: Wariller, C.: Allain, F.; Kouach, M.; Spik, G.
Blochim. Blophys. Acta 1293, 31-38, 1966
A.Title: Evidence that human milk isolated cyclophilin B corresponds to a truncated form A.Feference number: S65742; MUID: 96186273
A.Molecule type: protein
A.Molecule type: protein
A.Residues: 26-30; 203 <AMR>
A.Experimental source: milk
C.Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence C.Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence C.Comment: This protein binds to and is inhibited by the immunosuppressive drug cyclospc C.Goment: This protein binds to and is inhibited by the immunosuppressive drug cyclospc C.Goment: This protein binds to and is somerization of peptidylprolyl isomerase; cyclophilin homology
C.Gomention:
A.Description: catalyzes the cis-trans isomerization of peptidylprolyl isomerase; cyclophilin homology
C.Superfamily: peptidylprolyl isomerase; cyclophilin homology
C.Superfamily: spetidylprolyl isomerase B #status experimental cMAT>
F:1-25/Domain: signal sequence #status predicted
F:140/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Poptidylprolyl isomerase (EC 5.2.1.8) CyP-S1 precursor - mouse
N'Alternate names: cyclophilin B; cyclophilin-S1; cyclosporin A-binding protein
N'Alternate names: cyclophilin B; cyclophilin-S1; cyclosporin A-binding protein
C; Species: Mus musculus (house mouse)
C; Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Jul-1999
C; Accession: A66801; B3972; S21835
R; Schumacher, A.; Schroter, H.; Multhaup, G.; Nordheim, A.
Blochim. Blophys. Acta 1129, 13-22, 1991
A:Title: Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a putative sign
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C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
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R: Friedman, J.; Weissman, I.
Cell 66, 799-806, 1991
A; Ttiedman, J.; Weissman, I.
Cell 66, 799-806, 1991
A; Ttie: Two cytoplasmic candidates for immunophilin action are revealed %; Reference number: A40047; MUID:91347379
A; Accession: A40047
A; Accession: A40047
A; Molecule type: DNA
A; Residues: 1-212 <FRI>A; Molecule type: DNA
C; Comment: This protein binds the immunosuppressive drug cyclosporin A.
C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
C; Superfamily: cyclophilin homology <C; F; 37-199/Domain: cyclophilin homology <CYP>
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0.0.0076;
0; Indels
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100.0%; Pred. No. 0.C
ive 0; Mismatches
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Best Local Similarity 100.
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Best Local Similarity 100.

Matches 9; Conservative
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91 DFMIQGGDF
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A Residues 1. 216 <a href="#">A Report Imental Source: transcortinoms P9 cells</a>
A Residues 1. 216 <a href="#">A Report Imental Source: transcortinoms P9 cells</a>
A Report Imental Source: transcortinoms P9 cells
A Reference Extracted from World The April 2013.
A Reference of The Source: transcortinoms of the mature protein, were c Pendson and the Source: transcortinoms of the mature protein, were c Pendson and the Source: transcortinoms of the mature protein, were c Marchain.
A Reference number: A 19722; WID-91260697
A Reference number: S 20183
A Reference number: A 19722; WID-91260697
A Reference number: S 20183
A Reference number: A 19722; WID-91260697
A Reference number: A 19722; Reference number: A 19723; Reference number: A 19
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A; Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds A;Note: activity is one-tenth that of the mammalian protein; high binding affinity fo C; Superfamily: peptidylprolyl isomerase; cyclophilin homology C; Keywords: acetylated amino end; blocked amino end; cis-trans-isomerase; cyclosporin F;1-162/Domain: cyclophilin homology <CYP>
F;2-162/Product: peptidylprolyl isomerase, cytosolic #status experimental <MAT>
F;2-Modified site: acetylated amino end (Ser) (In mature form) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptidylprolyl isomerase (EC 5.2.1.8) - Streptomyces chrysomallus
N;Alternate names: cyclophilin A; cyclosporin A-binding protein
C;Species: Streptomyces chrysomallus
C;Species: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C;Accession: S28020; S25676
R;Pahl, A.; Uehlein, M.; Bang, H.; Schlumbohm, W.; Keller, U.
Mol. Microbiol. 6, 351-3558, 1992
A;Title: Streptomycetcs possess peptidyl-prolyl cis-trans isomerases that strongly re
A;Title: Streptomycetcs mumber: S28020; MUID:93116593
A;Accession: S28020.
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                                                               A;Gross-references: EMBL:Z50046; NID:g899393; PIDN:CAA90376.1; PID:g899403; GSPDB:GNO A;Experimental source: strain AB972
R;Hasumi, H.; Nishikawa, T.
                                                                                                                                                   R;Hasumi, H.; Nishikawa, T.
Biochim. Biophys. Acta 1161, 161-167, 1993
A;Title: Purification and properties of multiple molecular forms of yeast peptidyl pr
A;Reference number: S29645; MUID:93160233
A;Accession: S29645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptidylprolyl isomerase (EC 5.2.1.8) a, cytosollc - fungus (Fusarium sporo N;Alternate names: cyclophilin A C;Species: Fusarium sporotrichioides C;Species: Fusarium sporotrichioides C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 19-Jan-2001 C;Accession: JT0686; PNOIG6; JT0702 R;Chow, L.P.; Ueno, Y.; Tsugita, A. submitted to JIPID, June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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A; Residues: 1-165 <PAH>
A; Residues: 1-165 <PAH>
A; Cross-references: EMBL: 215137; NID:946835; PIDN:CAA78840.1; PID:946836
C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
C; Keywords: cis-trans-isomerase; cyclosporin A binding
F; 2-165/Domain: cyclophilin homology <CYP>
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A;Residues: 'X',3-8,'X',10;30-37;75-78;81-85;159-162 <HAS>
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0.015;
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88.9%; Pred. No. 0.015;
live 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: SGD:CPH1; MIPS:YDR155c
A;Cross-references: SGD:SO002562; MIPS:YDR155c
A;Map position: 4R
C;Function:
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Matches 8; Conserv
A; Molecule type: DNA
A; Residues: 1-162 <MUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.Alternate names: CARS-Cyp
C;Species: Homo sapiens (man)
C;Species: Toolwill, K.; Harper, S.; Pawson, T.; Anderson, S.K.
Gene 180, 151-155, 1996
A;Title: RS cyclophilins: Identification of an NK-TR1-related cyclophilin.
A;Reference number: JC5314; MUID:97128820
A;Andecule type: mRNA
A;Residues: 1-754 <NES>
A;Cross-references: EMBL:U40763; NID:91117967; PIDN:AAB40347.1; PID:91117968
A;Experimental source: thymus
A;Residues: Toole: thymus
A;Residues: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptidylprolyl isomerase (EC 5.2.1.8), cytosolic - yeast (Saccharomyces cerevisiae)
NiAlternate names: cyclophilin A: cyclosporin A-binding protein; peptidylprolyl isomeras
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 05-Nov-1999
C;Accession: 825443; J00125; 857980; 829645
R;Dietmeier, K.; Tropschug, M.
Nucleic Acids Res. 18, 373, 1990
A;Title: Nucleotide sequence of a full-length cDNA coding for cyclophilin (peptidyl-prol
A;Reference number: 825443; MUID:90221831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: $25443
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Cross-references: EMBL:X17505; NID:g3617; PIDN:CAA35545.1; PID:g3618
B;Haendler, B.; Keller, R.; Hiestand, P.C.; Kocher, H.P.; Wegmann, G.; Movva, N.R.
Gene B3, 39-46, 1989
A;Title: Yeast cyclophilin: isolation and characterization of the protein, cDNA and gene
A;Reference number: JQ0125; MUID:90076969
A;Accession: JQ0125
A;Accession: JQ0125
A;Accession: JQ0125
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A; Note: part of this sequence was confirmed by protein sequencing
K; Murphy, L.; Richards, C.; Harris, D.
submitted to the EMBL Data-Library, July 1995
A; Reference number: S57971
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                                   Length 260;
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                                       Score 50; DB 2; Length 26 Pred. No. 0.0096; Mismatches 0; Indels
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C;Superfamily: CARS cyclophilin; cyclophilin homology
F;7-177/Domain: cyclophilin homology <CYP>
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Pred. No. 0.052;
1; Mismatches
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                                           100.0%;
100.0%;
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Best Local Similarity 88.9%;
Matches 8; Conservative
                                       Ouery Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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A; Gene: GDB:CYP; CARS-CYP
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A; Molecule type: DNA
A; Residues: 1-172 <WIL>
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Best Local Similarity
Matches 8; Conserv
                                 66 EFMIQGGDF 74
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A: Description: Amino acid sequence of peptidyl-prolyl isomerase a from Fusarium sporotril
A: Reference number: J70686
A: Mocession: J70686
A: Mocession: J70686
A: Mocession: J70686
A: Molecule type: protein
A: Residueus: 1-179 CCH0>
B: Fukaya. N: Chow. L.P.: Sugiura, Y:; Tsugita, A.; Ueno, Y:; Tabuchi, K.
B: Fukaya. N: Chow. L.P.: Sugiura, Y:; Tsugita, A.; Ueno, Y:; Tabuchi, K.
A: Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A: Reference number: PN0160
A: Molecule type: protein
A: Residues: 1-41 cFuKA
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: Chow. L.P.: Kamo, M: Ueno, Y:; Tsugita, A.
R: L.P.: M: Chulled to JIPID, Levaled to Libration Residence of Peptidylprolyl isomerase. Pocific cPp.
F: 1179 Comann: cyclophilin homology cryp.
F: 1179 Comann: cyclophilin homology cryp.
F: 1187 Residues: Libration Residence (Ser) (covalent) (by protein kinase II) *status predicted F: 131/Binding site: Phosphate (Fr.) (covalent) (by protein kinase II) *status predicted F: 131/Binding site: Phosphate (Fr.) (covalent) (by casein kinase II) *status predicted F: 132/Binding site: Phosphate (Fr.) (covalent) (by casein kinase II) *status predicted F: 132/Binding site: Phosphate (Fr.) (covalent) (by Covalent) (by casein kinase) *status predicted F: 132/Binding site: Phosphate (Fr.) (covalent) (by Casein kinase
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Pred. No. 0.016;
1; Mismatches 0; Indels
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Best Local Similarity 88.9%; Pred. No. 0.04;
Matches 8; Conservative 1; Mismatches
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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70 DFMLQGGDF 78
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Peptidylprolyl isomerase (EC 5.2.1.8) ZK520.5 [similarity] - Caenorhabditis elegans N:Contains: cyclophilin C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000 C:Accession: T27882 R:Steward, C. Submitted to the EMBL Data Library, March 1997 A:Reference number: 220434 A:Reference number: 220434
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C.Superfamily: peptidylprolyl isomerase; cyclophilin homology

C.Keywords: cis-trans-isomerase

F.3-171/Domain: cyclophilin homology <CYP>
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Pred. No. (
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January 15, 2002, 13:05:27; Search time 81.32 Seconds (without alignments) 8.198 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ailidaoloxo aemaH	Human secreted oro	Human Cyclophilin	Human cyclophilin	Human Capora again	Himan colon canon	Himan EST encoded	Human Cyclophilin	Himan Cyclopitin	Arabidonsis thalia	Arabidopsis thalia
SUMMARIES	1D	AAY69923	AAG00090	AAB73302	AAB73301	AAB43878	AAG75931	AAM24287	AAY69924	AAU01197	AAG05073	AAG05072
	DB	21	21	22	22	21	22	22	21	22	21	21
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Claim 4; Page 50; 64pp; Japanese.

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ALIGNMENTS

Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy. Tumour antigen peptides derived from cyclophilin B for treatment and diagnosis of tumours $\,$ -Human cyclophilin B peptide fragment #3. AAY69923 standard; peptide; 9 AA. (SUMU) SUMITOMO PHARM CO LTD. 98JP-0178449. 99WO-JP03360. 11-APR-2000 (first entry) WPI; 2000-116932/10. Gomi S; (ITOH/) ITOH K. W09967288-A1. Homo sapiens 24-JUN-1999; 25-JUN-1998; 29-DEC-1999. AAY69923; Itoh K, AAY69923 RESULT a

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                                                                                                                                                                                                                                                                                                                        ; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs different propared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic. Gorensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
          sequence represents a cyclophilin B peptide of the invention. The
                      peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                              Gaps
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                                                                                                      100.0%; Score 51; DB 21; Length 9; 100.0%; Pred. No. 4.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.
                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                     Human secreted protein, SEQ ID NO: 4171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duclert A,
                                                                                                                                                                                                                                 AAG00090 standard; Protein; 166 AA.
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N-PSDB; AAC00096.
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                    1 GFGYKNSKF 9
                                                                      9 AA;
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                                                                                                                                                                                                                                                                                                                                     gene therapy;
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Score 51; DB 21; Length 166; Pred. No. 0.076;

100.0%;

Query Match Best Local Similarity

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The invention relates to a composition for modulating somatolactogenic function, comprising cyclophilin B (CypB), a mutant of cyclophilin B (cyclophilin B compromed are absent) or an inhibitor of the interaction of cyclophilin B with a composition of the interaction of cyclophilin B with a composition or an inhibitor of the interaction of cyclophilin B with a composition or also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic function in the animal, and cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic function in the animal. A composition comprising cyclophilin B is useful in the treatment of immunosuppression, in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising cyclophilin B mutant or a composition comprising cyclophilin B mutant or a composition comprising cyclophilin B with a somatolactogenic composition composi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; glgantism; acromegaly; hyperprolactinaemia; c-terminal deletion mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.
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Pred, No. 0.096;
                                                                                                                                                                                                                                                                                                                                                                    AAB73302 standard; protein; 211 AA.
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function, comprising cyclophilin B (CypB), a mutant of cyclophilin B (Particularly a CypB mutant in which residues 2-12 of the mature protein are absent) or an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone (e.g., prolactin, growth hormone). The invention also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, is useful for inhibiting somatolactogenic function in the animal. A composition comprising cyclophilin B with a somatolactogenic hormone, is useful for in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising cyclophilin B cyclophi
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cyclophilin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a composition for modulating somatolactogenic
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include: cytostatic; proliferative; unlnerary; immunomodulator; antiatheric; antiatherative; unlnerary; immunomodulator; antiatheratic; cagulant; concirole; assortopic; antiatheratic and antiangioganic. The controlections and polypeptides can be used for preventing, treating or ameliorating medical conditions and antianging stand antiagonists from the present invention may be used to treat immune disorders by activating to rinhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate haemostatic or thrombolytic activity, modulate baction, and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB4240 represent sequences used in the exemplification of the present invarior invarior.
                                                                                                                                                                                                                                                                                                                                                                                    dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                                                                                   Human: cancer associated gene; cancer antigen; detection; cancer;
diagnosis: cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antinheumatic; antiarthritic; antiviral;
antiinflammatory; antithyroid; antiallergic; antiboterial; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -
                                                                                                                                                                                                                                                        Human cancer associated protein sequence SEQ ID NO:1323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 1974-1975; 2352pp; English.
                                                                                                                         AAB43878 standard; Protein; 291 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2000; 2000WO-US05882
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N-PSDB; AAC78087
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                                                                                                                                                                     AAB43878;
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100.0%; Score 51; DB 22; Length 216; 100.0%; Pred. No. 0.099; ive 0; Mismatches 0; Indels (

Query Match 100.

Best Local Similarity 100.

Matches 9; Conservative

1 GFGYKNSKF 9

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ò 8 AAG75931

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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, veast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                          Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 83; 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Cao Y, Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 1183-1184; 1275pp; English.
                                                                                                                                                                                                                    Human EST encoded protein SEQ ID NO: 1812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.4%; Scur
100.0%; Pre
0; }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY69924 standard; peptide; 11 AA.
                                                                                                 AAM24287 standard; Protein; 83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2001; 2001WO-US02687
                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein of the invention.
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Best Local Similarity
7; Conserv?
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94 gygykgskf 102
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77 gfgykns 83
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                                                                                                                                                                                                                                                                                                                                                                Homo saptens
                                                                                                                                                                               12-OCT-2001
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                                                                                                                                           AAM24287;
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1D AAY6;

XX

AC AAY6;

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DT 11-A;
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AAM24287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                      Gaps
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N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                     Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma.
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                      Indels
                                                                                                                                                                                                                                                                                                                          Human colon cancer antigen protein SEQ ID NO:6695.
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Pred. No. 2.2;
1; Mismatches 1
    100.0%; Pred. No. 0.13; ive 0; Mismatches
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                                                                                                                                                                                                     AAG75931 standard; Protein; 112 AA.
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Best Local Similarity 77.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0157137
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                                                                                                                                                                                                                                                                                   (first entry)
    Best Local Similarity 100.
Matches 9; Conservative
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N-PSDB; AAH35336.
                                                                                     112 AA;
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                                                              1 GFGYKNSKF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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03-NOV-1999;
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Gaps

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us-09-720-469-3.rag

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The present sequence represents human cyclophilin D which is a mitochondrial core component. Cyclophilins interact with other commonants core components e.g. adenine nucleotide translocator (ANT) proteins to regulate MPT. ANT proteins are mitochondrial permeability transport to proteins to regulate MPT. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial concent protein (EFM) protein (e.g. ANT) fused to an energy transfer molecule (EFM) protein (e.g. ANT) fused to an energy transfer component polypeptide (e.g. ANT) fused to an energy transfer component polypeptide (e.g. ANT) fused to an energy transfer concentration (e.g. and protein (e.g. and protein for a protein (e.g. and protein (e.g. and protein for a                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                 New nucleic acid expression constructs, useful for screening for agents
                                                                                                  that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule
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Pred. No. 14;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG05073 standard; Protein; 254 AA.
                                                                                                                                                                         Disclosure; Fig 8; 186pp; English.
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990S-0123180.
990S-012548.
990S-0126264.
990S-0126785.
990S-0126785.
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77.8%;
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Matches 7; Conservative
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                            WPI; 2001-291054/30
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                                             N-PSDB; AAS05937
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05-MAR-1999;
09-MAR-1999;
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; adenine nucleotide translocator; ANT; MTP; cyclophilin D; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                  Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                       Tumour antigen peptides derived from cyclophilin B for treatment and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.5%; Score 39; DB 21; Length 11; 100.0%; Pred. No. 0.73; 0; Indels ive 0; Mismatches 0; Indels
Human cyclophilin B peptide fragment #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU01197 standard; Protein; 207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 50; 64pp; Japanese.
                                                                                                                                                                                                                                                                           (SUMU ) SUMITOMO PHARM CO LTD
                                                                                                                                                                                                                                         98JP-0178449.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murphy AN, Clevenger W,
Velicelebi G, Davis RE;
                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis of tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AA;
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                                                                                                                                                                                                                                                                                             (ITOH/) ITOH K.
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1 gyknskf 7
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                                                                                             Homo sapiens
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Best Local S
Matches 7
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19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 20-JUL-1999; 20-JUL-1999;	20-JUL-1999; 21-JUL-1999;	21-JUL-1999; 21-JUL-1999;	22-JUL-1999; 22-JUL-1999;	22-JUL-1999; 22-JUL-1999;	23-JUL-1999;	23-JUL-1999; 23-JUL-1999;	26-JUL-1999;	27-JUL-1999; 27-JUL-1999;	27 - JUL - 1999;	28-JUL-1999; 02-AUG-1999;	02-AUG-1999;	02-AUG-1999; 03-AUG-1999;	04-AUG-1999;	04-AUG-1999;	05-AUG-1999;	06-AUG-1999;	06-AUG-1999;	09-AUG-1999;	10-AUG-1999;	11-AUG-1999;	13-AUG-1999;	13-AUG-1999;	16-AUG-1999; 17-AUG-1999;	18-AUG-1999;	20-AUG-1999;	20-AUG-1999;	23-AUG-1999;	23-AUG-1999;	26-AUG-1999;	27-AUG-1999;	27-AUG-1999;	30-AUG-1999;	31-AUG-1999; 01-SEP-1999;	07-SEP-1999;	10-SEP-1999;	15-SEP-1999;	16-SEP-1999;	22-SEP-1999;	23-SEP-1999;	24-SEP-1999;	29-SEP-1999;	04-OCT-1999;	05-OCT-1999; 06-OCT-1999;	07-0CT-1999;	12-0CT-1999;	13-0CT-1999;	13-0CT-1999;
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0128714. 0129845. 0130077. 0130449.	130891.	132048. 132407.	132484. 132485.	132486.	132863.	134256. 134218.	134219.	134221.	134768.	134941. 135124.	135353.	135629.	136392.	136782.	13/222.	137502.	137724.	138094.	138847.	139119.	139452.	139492.	139454.	139456.	139457.	139459.	139460.	139461.	139463.	139750.	139817.	139899.	140353.	140695.	140823.	141287.	141842.	142154. 142055	142390.	142803.	142977.	143542.	143624.	144085.	144086.	144331.	144332.
99US-012 99US-012 99US-013 99US-013	0-S066	0-8066	990S-0	0-S066	0-sn66	0-S066	990S-0	0-8066	0-sn66	0-8066	0-8066	0-8066	0-sn66	0-sn66	0-5066	0-S066	0-Sn66	0-5066	0-SD66	0-Sn66	0-S066	0-sn66	0-8066	0-S066	0-8066	0-8066	0-S066	9908-0	0-S066	0-S066	0-8066	0-Sn66	0-8066	0-8066	0-5066	0-S066	0-S066	0-8066	0-S066	0-S066	0-S066	0-S066	0-8066	0-S066	0-S066	0-S066	0-8066
1999; 1999; 1999; 1999;	1999;	1999;	1999; 1999;	1999; 1999;	1999;	1999; 1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;
08-APR-1999; 16-APR-1999; 19-APR-1999; 21-APR-1999; 23-APR-1999;	23-APR- 28-APR-	30-APR- 30-APR-	04-MAY- 05-MAY-	06-MAY-	07 - MAY -	11-MAY- 14-MAY-	14-MAY-	14-MAY- 14-MAY-	18-MAY-	19-MAY- 20-MAY-	21 - MAY -	24 - MAY - 25 - MAY -	27 - MAY -	28-MAY-	-NOO-TO	04 -JUN-	-NUL-70	-NOC-80	10-JUN-	14-JUN-	-NOC-91	17-JUN-	18-JUN-	18-JUN-	18-JUN-	18-JUN-	18-JUN-	18-JUN-	18-JUN-	18-JUN-	21-JUN-	22-JUN-	23-JUN- 23-JUN-	24-JUN-	28-JUN-	30-JUN-	01-JUL-	-70F-70 -7111-	06-JUL-	- 70L-80	12-JUL-	13-JUL-	14-JUL-	16-JUL-	16-JUL- 19-JUL-	19-JUL-	19-JUL-
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                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No.
                                                                                                                                                                                                                                                                            AAG05072 standard; Protein; 259 AA
990S-0159295.
990S-0159329.
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990S-0159638.
990S-0160761.
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77.8%;
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99US-0162142.
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
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9908-0151086
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9908-0154018
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990S-0145086.
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99US-0151065
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12-AUG-1999;
13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
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27-JUL-1999;
27-JUL-1999;
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18-OCT-1999,
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23-AUG-1999
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01-SEP-1999
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22-SEP-1999
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02-AUG-19
02-AUG-19
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05-AUG-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection and therapy of cervical cancer - using specific cervical cancer-associated proteins as targets for treatment or as indicators for detection
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cervical cancer-associated protein; CvC; tryptic peptide; human; detection; treatment; Nup358; nucleoporin; non-chromatin protein.
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                                                                                                                                                                                                                                     21; Length 259;
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17;
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                                                                                                                                                                                                                                    Score 39;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                     AAW54235 standard; peptide; 3224 AA.
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                                                                                        990S-0160989.
990S-0161404.
990S-0161405.
990S-0161359.
990S-0161359.
       990S-0160767.
990S-0160768.
990S-0160814.
99US-0160815.
99US-0160981.
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99US-0161992.
99US-0161993.
99US-0162142.
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77.88;
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                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MATR-) MATRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Nup358 protein.
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                                                                                                                                                                                                                                                Best Local Similarity
Matches 7; Conser
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21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
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25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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28-OCT-1999;
28-OCT-1999;
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                                                                                                                                                                                                                                        Query Match
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human secreted proteins given in AAF33037 to AAF33085 encode the human secreted proteins given in AAB64666 to AAB64714. AAB64715 to AAB6471 represent human secreted polypeptide sequences and proteins composed to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues condition. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: continifiamments; antiarthritis; dermalogical; cardiant: antialinflamments; antiarthritis; and anti-ulcer. The polynucleotides and polypeptides can be used in the prevention, treatment and diagnosis of diseases associated with inappropriate polypeptide expression. Disorders that may be treated or prevented include solid tumours, conformation arthritis, psoriasis, diabetic retinopathy, myocardial conjugementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and therefore which patients may be in need of restorative therapy. The polypeptides
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cervical cancer cell than in a normal human cervical cell, as determined by 2D-gel electrophoresis. The methods can be used for the early and rapid detection of cervical cancer, for treating cervical cancers and for monitoring the efficacy of such treatment.
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; diagnosis; cytostatic; antirheumatic; antiarthritic; dermalogical; cardiant; antiinflammatory; anti-ulcer; gastrointestinal; solid tumour; rheumatoid arthritis; psoriasis; diabetic retinopathy; myocardial anglogenesis; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding 49 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases such as tumors, rheumatoid arthritis, psoriasis and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein sequence encoded by gene 14 SEQ ID NO:131.
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                                                                                                                                                               Length 3224;
                                                                                                                                                           Score 39; DB 19; Length 32
Pred. No. 2.2e+02;
1; Mismatches 1; Indels
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                                                                                                                                                             76.58;
77.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2000; 2000WO-US14928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                             Query Match 76.5
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                   3224 AA
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                                                                                                   Sequence
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may also be used as antigens in the production of antibodies against the polypeptide and in assays to identify modulators (agonists and antagonists) of polypeptide expression and activity. The anti-polypeptide antibodies and antagonists may also be used to down regulate expression and activity. AAF33028 to AAF33036 and AAB64665 represent sequences used in the exemplification of the present invention.
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria gonorrhoeae Protein I gene sequences sed for detection of N. gonorrhoea infection and producing vaccines for prevention or treatment of infection
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                                                                                                                                                                                                                                                                                                                                              Neisseria gonorrhoea (NG); NG strain FA19; peptide sequence;
                                                                                                                      22; Length 114;
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Pred. No. 32;
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12;
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                                                                                                                   Score 38;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                        Protein IA of N. gonorrhoea strain FA19.
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/label= signal-peptide
                                                                                                                                                                                                                                                   315 AA.
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                                                                                                                   74.58;
77.88;
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77.88;
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                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 77.0.
                                                                                                                                            7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Neisseria gonorrhoea.
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N-PSDB; AAN90047.
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                                                                                  114 AA;
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                                                                                                                                                                                                                                                                                                                                                            Protein IA.
                                                                                                                                                                                                                                                                         AAP90099;
                                                                                Sequence
                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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The sequence given is encoded by the protein IA gene of Neisseria gonorrhoeae. PIA is a major outer membrane proteins of N. gonorrhoeae which act as a porin. Porins are believed to act in cells by channelling low molecular weight substances across the hydrophobic lipid outer membrane. Elucidation of the gene sequences of PIA and PIB allows the production of antiganic fragments by recombinant DNA techniques. These fragments can be used as immunogens in vaccine compositions for the prevention of gonorrhoea, and also on immunoassays for diagnosis of infection. See also AAR27484.
                                                                                                                                   Protein IB; PIB; Neisseria gonorrhoeae; PIA; outer membrane; porin; hydrophobic; lipid; outer membrane; antigen; immunogen; vaccine; gonorrhoea; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fragments of Neisseria Gonorrhoeae protein IA or IB – used as vaccines for preventing gonorrhoeal infection, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Length 315;
                                                                                                                                                                                                                              1..18
/label= Signal_peptide
19..315
/label= Mature_protein
                                                                                                                                                                                                                   Location/Qualifiers
                            AAR27483 standard; Protein; 315 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 3; 95pp; English
                                                                                                                                                                                                                                                                                                                                                    92WO-US02006
                                                                                                                                                                                                                                                                                                                                                                              91US-0669492
                                                                                                                                                                                                                                                                                                                                                                                                         (UYNC-) UNIV NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sparling FP;
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-348935/42.
N-PSDB; AAQ29138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 315 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Carbonetti N,
                                                                                                                                                                                                                                                                                                                                                    13-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                             14-MAR-1991;
                                                                                                                                                                                                                                                                                                 WO9216223-A.
                                                                                 08-MAR-1993
                                                                                                                                                                                                                                                                                                                           01-OCT-1992
                                                                                                           Protein IA
                                                                                                                                                                                          Synthetic
                                                      AAR27483;
                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                          Protein
RESULT 15
AAR27483
                                                                                                                                                                                                                    Key
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Search completed: January 15, 2002, 13:05:27 Job time: 198 sec

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Gaps

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Indels

74.5%; Score 38; DB 77.8%; Pred. No. 32; tive 0; Mismatches

Best Local Similarity 77.8 Matches 7; Conservative

Query Match

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100.0%; Score 51; DB 2; Length 126; 100.0%; Pred. No. 0.017; ive 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 781-1989
TELEFA: (415) 398-3249
TELERA: 910 277299
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 amino acids
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Best Local Similarity luv...
9; Conservative
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Sequence 11, Appl
Sequence 8, Appli
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5.381 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                     Search time 37.64 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-451-747-13
US-08-134-852-13
US-08-142-897-8
US-08-145-995A-9
US-08-411-747-9
US-08-411-747-9
US-08-482-728A-12
US-08-989-045-34
US-08-989-045-34
US-08-482-728A-15
US-08-482-728A-15
US-08-482-728A-9
US-08-482-728A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-944-604-20
US-08-944-604-18
US-08-142-897-5
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
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51
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                                                                                                                                                                                                                Title:
Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                           Sequence:
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Sequence 9, A
Sequence 14,
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Sequence 19,
Sequence 19,
Sequence 19,
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Sequence 4,
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21
US-08-096-182A-2
US-08-877-109-2
US-08-877-109-2
US-08-877-2
US-08-142-728A-16
US-08-145-995A-14
US-08-451-747-14
US-08-451-747-14
US-08-451-747-14
US-08-459-351-19
US-08-459-351-19
US-08-460-533-19
US-08-460-533-19
US-08-460-533-19
US-08-460-533-10
US-08-259-672-6
US-08-460-533-6
US-08-460-533-6
                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                           US-08.482-728A-10; Sequence 10, Application US/08482728A; Patent No. 5968802; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 596
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'RY: United States 94111-4187
  3309
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1162
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ADDRESSEE: DAVID G. CONLIN: DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
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Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/08451747 Patent No. 5821107
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEE: 200291 STRE UR
INFORMATION FOR SEO ID NO: 13
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.2%;
                                                130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 161 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 88.2
Best Local Similarity 88.9
Matches 8; Conservative
                                                                               STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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42 GFGYKGSKF 50
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                                                STREET: 130 W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01915
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                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Welssman, Jeffrey S.
APPLICANT: Welssman, Irving L.
TITLE OF INVENTION: NO. 5447852el Cyclophillins, Associating Proteins TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Patent No. 5482850
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-400-1991
ATTONNEY, AGENT INFORMATION:
NAME: Dunn, Tracy D.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                           Sequence 7, Application US/08142897
Patent No. 5447852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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          28 GFGYKNSKF 36
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                                                                                                                                                                                                                                                                                                                                                                                                           94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-145-995A-13
                                                                                       RESULT 2
US-08-142-897-7
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STREET: 32 TOZER ROAD
CITY: BEVERLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DEADER FLOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: RESMICK, DAVID S.
REGISTRATION NUMBER: 34.235
REFERENCE/POCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
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Gaps

; 0

ATTORNEY/AGENT INFORMATION:

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RESULT 7
US-08-142-897-8
Sequence 8, Application US/08142897
Factor No. 5447852
GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
                                                 Score 45; DB 3; Length 161;
Pred. No. 0.27;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 126; 0.76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                        No. 5968802el Nuclear Cyclophilin
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclop)
NUMBER OF SEQUENCES: 21
CORRESSEDE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: Flehr, Hobbach, Test, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 2
Pred. No. 0.76;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A-61230/DJB/RMS
                                                                                                                                                                                                                                                    Sequence II, Application US/08482728A; Patent No. 5968802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFRENCE/DOCKET NUMBER: A-61;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                 88.2%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.48;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 amino acids
                                           Query Match 88.2
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RY: United States 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.4
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-482-728A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
COUNTRY: United St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                             ||||| ||| 42 GFGYKGSKF 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1:111 | 111
28 GYGYKGSKF 36
                                                                                                                        1 GFGYKNSKF 9
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                                                                                                                                                                                                              RESULT 6
US-08-482-728A-11
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Patent No. 6127148
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: GUSHNAN
                                                                                                                                                                                                                                                                                                                                             DB 2; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
                                                                                                                                                                                                                                                                                                                                           Score 45; DB 2
Pred. No. 0.27;
0; Mismatches
                                                       NEB-046-DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-CCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLTAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-
TELECOMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
NEDOCULE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:

TELEFAX: (617) 523-3400
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
STAMNEDBRESS: unknown
TOPOLOGY
                                                                                                                                        INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 161 amino acids TYPE: amino acid STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REGISTRATION NUMBER: 43.
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                         88.2%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 130 WATER STREET CITY: BOSTON STATE: MASSACHUSETTS COUNTRY: USA
                                                                                                                                                                                                                  ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-451-747-13
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GFGYKNSKF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-134-852-13
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.3;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
29-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-00T-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WILLYAMS, GREGORY D.
REGISTRATION NUMBER: 30901
                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 3425
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-640
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 9, Application US/08451747; Patent No. 5821107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.4%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ 1D NO: 5
SEQUENCE CHARACPERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                    164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 78.4 Best Local Similarity 77.8 Matches 7; Conservative
                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-145-995A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 GFGYKGSSF 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-08-451-747-9
                                                                                                                                                                                                                                                                                                                    LENGTH:
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US-08-145-995A-9
Sequence 9, Application US/08145995A
Sequence 9, Application US/08145995A
Factor No. 5482850
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PACE, ANTON:
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS 6
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS 6
ADDRESSEE: DAVID G. COLITY: BASSACHUSETTS
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                 TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dun
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                        COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1
Pred. No. 2.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: 34.587
RECISTRATION NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.4
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-142-897-8
                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 GFGYKGSSF 52
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STATE:
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                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09134852

Patent No. 6127148

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STREET: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                            DB 2; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.4%; Score 40; DB 3; Length 164; 77.8%; Pred. No. 2.3; Live 0; Mismatches 2; Indels
                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/09/134,852
                                                                                                            Score 40; DB 2
Pred. No. 2.3;
                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34.35
REFERENCE/DOCKET NUMBER: 434.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523.3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
                                                                                                            78.48;
77.88;
                                                                                                       Query Match
Best Local Similarity 77.8
Matches 7; Conservative
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
               TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-451-747-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                      11111 | |
45 GFGYKGSSF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 GFGYKGSSF 53
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                                                                                                                                                                                                                                                                            RESULT 10
US-09-134-852-9
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RESULT

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                              GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Pisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr, Hobbach, Test, Albritton
ADDRESSE: 6 Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
STREET: ADDRESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/08705660
Fatent No. 585863
GENERAL INFORMATION:
APPLICANT: RESEE. SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DETECTION OF CERVICAL CANCER
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION NOTE:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB;
Pred. No. 2.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A-61230/DJB/RMS
Sequence 12, Application US/08482728A Patent No. 5968802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: S11va, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61;
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 781-1989
TELEX: 910 277299
INFORMATION FOR SEO ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.58;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 77.00,
...a 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11111 | 1
28 GFGYKGSTF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFGYKNSKF 9
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US-08-705-660-34
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                                                                                               Length 3224;
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                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Silva, Robin M.
RECISTRAION NUMBER: 36,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 398-3249
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TENDTH: 126 amino acids
                                                                                             Score 39; DB 3;
Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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Pred. No. 6.2;
0; Mismatches
                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                       ; Sequence 15, Application US/08482728A ; Patent No. 5968802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08482728A; Patent No. 5958802 celebration Information: GENERAL INFORMATION: APPLICANT: Wang, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.58;
77.88;
                                                                                               76.5%;
                                                                        Ouery Match
Best Local Similarity 77.0°
نمو 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States ZIP: 94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-482-728A-15
; MOLECULE TYPE: peptide US-08-989-045-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                RESULT 14
US-08-482-728A-15
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US-08-482-728A-9
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Pred. No. 66;
1; Mismatches 1; Indels
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APPLICANT: OBAR, ROBERT
APPLICANT: OBAR, ROBERT
APPLICANT: WIN, YING-JYE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DETECTION OF CERVICAL CANCER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...LUIUM TYPE: _____ rOKM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,045
FILING DATE:
CLASSIFICATION:
ATTORNEY APPLICATION:
         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,660
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GREENMALGH, DUNCAN A
REGISTRENCE/DOCKET NUMBER: 38,678
REFRENCE/DOCKET NUMBER: 38,678
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 110PRAMATION:
TELECOMMUNICATION 1248-71000
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHRARCTERISTICS:
LENGTH: 3224 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/ACENT INFORMATION:
NAME: GREENHALGH, DUNCAN A
REGISTRATION NUMBER: 38,678
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPHONE: (617) 248-7000
TELEPHONE: (617) 248-7100
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/08989045 Patent No. 6027905 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.5
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3105 GFGFKNSIF 3113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GFGYKNSKF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ā
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US-08-989-045-34
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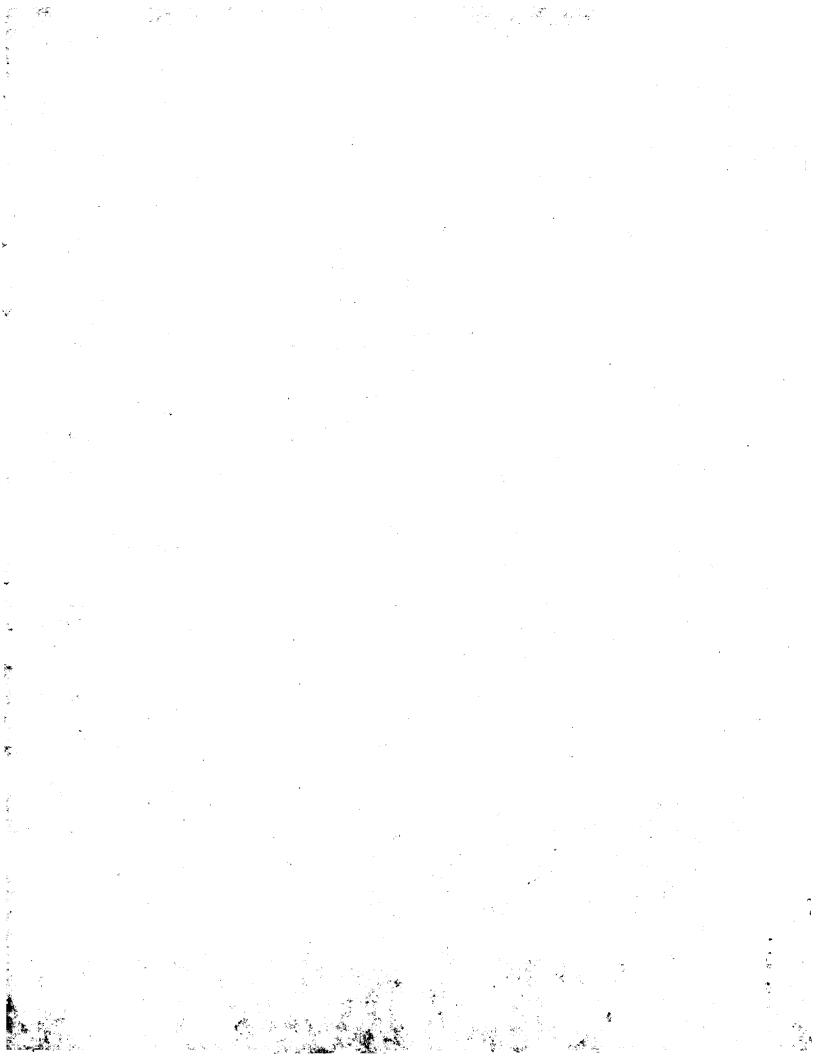
Gaps

```
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr, Hebbech, Test, Albritton
ADDRESSE: Flehr, Hebbech, Test, Albritton
STREET: Four Embarcadero Center, Suite 3400
STATE: California
COUNTY: United States
2.19 94111-4187
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC Compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
PERLETATION NUMBER: 195/80/482.728A
CLASSITCATION NUMBER: 195/80/482.728A
ATTORREY ADDIN 4.15-784.199
FILING DATE: OT-10N-1995
CLASSITCATION NUMBER: A61230/DJB/RMS
FELERAX: (415). 781-189
FELERAX: (415). 781-189
FELERAX: (415). 398-232
FELERAX: (415). 398-234
FELERAX: (415). 398-249
FELERAX: (415). 398-24
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Search completed: January 15, 2002, 13:03:59 Job time: 215 sec

1 GFGYKNSKF 9 |||||| | 1 28 GFGYKGSCF 36

Oy Db



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January 15, 2002, 13:06:15 ; Search time 42.04 Seconds (without alignments) 16.308 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                   219241 seqs, 76174552 residues
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                US-09-720-469-3
51
                                                                                                                                                                                                                     1 GFGYKNSKF 9
                                                                                                                                                                                                                                                            BLOSUM62
                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                         Sednence:
                                                                                                                                                                                                                                                                                                                   Searched:
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%

Total number of hits satisfying chosen parameters:

Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* PIR 68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

peptidylprolyl iso peptidylproly outer membrane pro hypothetical prote lectin-like adhesi peptidylprolyl peptidylprolyl peptidylprolyl peptidylprolyl peptidylprolyl peptidylprolyl peptidylprolyl peptidylprolyl Description SUMMARIES CSHUB A56861 A45000 S63995 A54204 A40516 A40516 A56814 CSHYAC CSMYAC CSMYAC CSMYAC CSBOAB CSNCM S68767 A41581 S58884 S24202 A39951 PC4425 CSHUA B38388 S51497 S71849 S71547 % Query Match Length DB Score Result Š.

hypothetical prote	2-hvdroxymuconate-	2-hydroxymuconate-	probable ribose/da	prolinetRNA liga	hypothetical prote	penicillin-binding	genome polyprotein	phosphodlycerate m	hypothetical prote	peptidylprolyl iso		outer membrane pro		nembrane	membrane
T21487	T31275	JC5419	D70184	G86890	F72393	JH0438	JQ1895	н81387	D82882	S28020	A40047	S25509	S25508	S25507	S25506
7	~	Н	Н	~	7	7	-	7	~	7	7	7	7	7	7
795	283	286	536	616	707	864	3163	492	121	165	212	293	294	295	295
9.07	68.6	9.89	68.6	9.89	9.89	9.89	9.89	9. 79	66.7	66.7	66.7	66.7	66.7	66.7	66.7
36	35	35	35	35	35	35	35	34.5	34	34	34	34	34	34	34
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

1 GFGYKNSKF 9 ò q

RESULT

peptidylprolyl isomerase (EC 5.2.1.8) B precursor [validated] - human N.Alternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin C; Species: Home sapiens (man) C. Species: Home sapiens (man) C. Sate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Dec-2000 C; Accession: A39118; A39722; A40515; S65742 R; Price, E.R.; Zydowsky, L.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T. Proc. Natl. Acad Sci. U.S.A. 88, 1903-1907, 1991 A; Title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl iso A; Reference number: A39118, MUID:91156714

A; Molecule type: mRNA A; Residues: 1-208 < PRID A; Cross-references: GB-M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335 A; Cross-references: GB-M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335 B; Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G. Mol. Cell. Biol. 11, 3484-3491, 1991 Mol. Cell. Biol. 11, 3484-3491, 1991 A; Title: An endoplasmic reticulum-specific cyclophilin. A; Reference number: A39722; MUID:91260697

iso

A;Molecule type: mRNA A;Residues: 1-208 <HAS> A;Cross-references: GB:M60457; NID:9181249; PIDN:AAA35733.1; PID:9181250

Gaps

0;

Indels

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Ricightowlers, M.W.; Haralambous, A.; Rickard, M.D.
Ricightowlers, M.W.; Haralambous, A.; Rickard, M.D.
Mol. Biochem. Parasitol. 36, 287-289, 1989
A;Titler Anthoo acid sequence homology between cyclophilin and a cDNA-cloned antigen o A;Reference number: A45000; MUID:90014983
A;Accession: A45000
                                                 A. Molecule type: mRNA
A. Residues: 9-216 < NRNA
A. Residues: 9-216 < NRNA
A. Cross-references: EMBL:X58990; NID:953034; PIDN:CAA41736.1; PID:953035
A. Cross-references: EMBL:X58990; NID:953034; PIDN:CAA41736.1; PID:953035
C. Comment: This protein is distinguished from peptidylprolyl isomerase A by the prese
C. Superfamily: peptidylprolyl isomerase; cyclophilin homology
C. Keywords: cis-trans-isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell
F:1-137/Domain: signal sequence #status predicted <SIG>
F:34-216/Product: peptidylprolyl isomerase B #status predicted <MAT>
F:43-205/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptidylprolyl isomerase (EC 5.2.1.8) [similarity] - tapeworm (Echinococcus granulosu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Contains: cyclophilin
C;Species: Echinococcus granulosus
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 08-Sep-2000
C;Accession: A45000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 51; DB 2; Length 216; 100.0%; Pred. No. 0.026;
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88.9%;
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-164 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-161 <LIG>
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Nylternate names: cyclophilin B: cyclophilin-S1: cyclosporin A-binding protein
C;Species: Mus musculus (house mouse)
C;Date: 05-Van-1996 #sequence_revision 05-Jan-1996 #text_change 16-Jul-1999
C;Accession: A56861: B39722; S21835
R;Schumacher, A: Schroter, H: Multhaup, G.; Nordheim, A.
Biochim. Blophys. Acta 1129, 13-22, 1991
A;Title: Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a putative sign A;Reference number: A56861; MUID:92096454
A;Reference number: A56861; MUID:92096454
A;Molecule type: mRA
A;Residues: 1-216 cSCH>
A;Experimental source: teratocarcinoma F9 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:73234, NCBIP:73239)
A;Note: sequence extracted from NCBI backbone (NCBIN:73234, NCBIP:73239)
A;Note: parts of this sequence, including the anino end of the mature protein, were conf
R;Hasel, K. W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
A;Reference number: A39722; MUID:91260697
A;Reference number: A39722; MUID:91260697
A;Residues: 9-216 cMRA
A;Residues: B-216 cMRA
A;Residues: B-216 cMRA
A;Residues: B-216 cMRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 26-30;203 <AMRNA
A; Repetimental source: milk
C; Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence
C; Comment: This protein binds to and is inhibited by the immunosuppressive drug cyclosper
C; Genetics:
A; Ge
presence
cyclospo
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R;Nordheim, A.
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Pred. No. 0.025;
0; Mismatches 0; Indels
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A;Reference number: S21835
A;Accession: S21835
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Best Local Similarity luv...
9, Conservative
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77 GFGYKNSKF 85
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peptidylprolyl isomerase (EC 5.2.1.8) - German cockroach
N.Alternate names: cyclophilin
C.Species: Blattella germanica (German cockroach)
C.Species: 10-701-1996 #sequence_revision 13-mar-1997 #text_change 20-Jun-2000
C.Accession: 563995
R.Martinez-Gonzalez, J.; Hegardt, F.G.
Bur. J. Blochem. 24, 284-292, 1995
Bur. J. Blochem. 24, 284-292, 1995
A.Title: Characterization of a cDNA encoding a cytosolic peptidylprolyl cis-trans-iso
A.Reference number: 563995; MulD:96096751
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                                                                                                                                                                                                                                                                                 Gaps
A;Cross-references: GB:J04664; NID:g158843; PIDN:AAA29058.1; PID:g158844 CS:Superfamily: peptidylprolyl isomerase: cyclophilin homology C;Keywords: cis-trans-isomerase cyclophilin homology F;1-161/Domain: cyclophilin homology <CYP>
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                                                                                                                                                                                                         Score 45; DB 2;
Pred. No. 0.26;
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C; Accession: A56814
R; Davis, T.R.; Tabatabai, L.; Bruns, K.; Hamilton, R.T.; Nilsen-Hamilton, M.
Biochim. Biophys. Acta 1095, 145-152, 1991
A; Title: Basic fibroblast growth factor induces 3T3 fibroblasts to synthesize and sec A; Reference number: A56814; MUID: 92031730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds C; Superfamily: peptidylprolyl isomerase; cyclophilin homology C; Keywords: cis-trans-isomerase; cyclosporin A binding; T-cell F; 3-164/Domain: cyclophilin homology <CYP>
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C; Species: Cricetulus griseus (Chinese hamster)
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C; Accession: S07597.
R; Bergsma, D.J.; Sylvester, D.
Nucleic Acids Res. 18, 200, 1990
A; Reference number: S07597; MUID:90174932
A; Recession: S07597
A; Molecule type: mRNA
A; Rocksion: S07597
A; Molecule type: mRNA
A; Residues: 1-164 < RER>
                                                              peptidylprolyl isomerase (EC 5.2.1.8) [similarity] - mouse (fragments) N.Alternate names: cyclophilin homolog SIP24 C;Species: Mus musculns (house mouse) C;Species: Aug-1995 isequence_revision 25-Aug-1995 isequence_revision 25-Aug-1995 #text_change 02-Sep-2000
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N;Alternate names: cyclophilin A; cyclosporin A-binding protein A
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar.1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: S10327, S66416; S40742
R;Hasel, K.W.; Sutcliffe, J.G.
Nucleic Acids Res. 18, 4019, 1990
A;Title: Nucleotide sequence of a cDNA coding for mouse cyclophilin.
A;Reference number: S10327; MUID:90326555
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                                                                                                                                                                                                                                                                                                                                                                                                                   A:Experimental source: BALB/c 3T3 cells
A;Note: sequence modified after extraction from NCBI backbone
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans'isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 38
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Pred. No. 0.54;
0; Mismatches
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Pred. No. 2.4;
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77.88;
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Best Local Similarity 77.6
Free 7: Conservative
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-38 < CDAV>
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                              C; Species: Homo sapiens (man)
C; Date: 22-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C; Date: 22-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C; Accession: A54204
R; Schneider, H; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurini, M.G.; Quesniau Blochemistry 33, 8218-8224, 1994
A; Title: Human cyclophilin C: primary structure, tissue distribution, and determination A; Reference number: A54204
A; Accession: A54204
A; Accession: A54204
A; Status: preliminary
A; Wolecule type: mRNA
A; Residues: 1-212 < SGH>
A; Cross-references: GB:S71018; NID:9547303; PIDN:AAB31350.1; PID:9547304
A; Experimental source: kidney
A; Note: sequence extracted from NCBI backbone (NCBIN:149387, NCBIP:149388)
A; Genetics:
A; Genetics: A54204
A; Genetics: CBB:136196; OMIM:123842
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C. Species: Gallus gallus (chicken)
C. Species: Gallus gallus (chicken)
C. Species: Gallus gallus (chicken)
C. Species: Gallus gallus (chicken)
C. Accession: A4016
R. Caroni, P.; Rothenfluh, A.; McGlynn, E.; Schneider, C.
J. Bloi. Chem. 266 10739-10742, 1991
A. Halo: Chem. 266 10739-10742, 1991
A. Reference number: A40516; MulD:91250364
A. Accession: A40516
A. Status: preliminary
A. Molocule type: mRNA
A. Residues: 1-207 < CAR
A. Residues: 1-207 < CAR
A. Residues: 1-207 < CAR
A. Cross-references: GB M63553; NID:9212648; PIDN:AAA49064.1; PID:9212649
C. Superfamily: peptidylprolyl Isomerase; cyclophilin homology
C. Keywords: cis-trans-isomerase; cyclophilin homology
C. Keywords: cis-trans-isomerase; cyclosporin A binding
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N:Alternate names: cyclophilin C
C:Species: Homo sapiens (man)
C:Date: 22-Oct:1994 *sequence_revision 18-Nov-1994 *text_change 16-Jul-1999
                                       Gaps
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                                 Indels
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C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase; cyclosporin A binding
F;37-199/Domain: cyclophilin homology <CYP>
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77.8%; Pred. No. 1.3;
Live 1; Mismatches 1
     ed. No. 0.98;
Mismatches
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Matches 7; Conserv
Best Local Similarity
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Best Local Similarity
Matches 7; Conserv
                                                                                                              79 GYGYKGSKF 87
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A Molecule type: Protein
A Residues: 1-179 < CH2>
Cicoment: This enzyme catalyzes interconversion of the cis and trans intho peptide b
C; Comment: This enzyme catalyzes interconversion of the cis and trans into peptide b
C; Comment: This enzyme catalyzes interconversion of the cis and trans into peptide b
C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
C; Keywords: cis-trans-isomerase; cyclosportin A binding; cytosol; nucleotide binding;
F; 1-179/Domain: cyclophilin homology cCYP>
F; 81-88/Region: nucleotide-binding motif A (P-loop)
F; 81-88/Region: nucleotide-binding motif A (P-loop)
F; 23.712/Binding site: phosphate (Thr) (covalent) (by casein kinase C) #status predicted
F; 23.78 hinding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F; 23.78 hinding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F; 132/Rinding site: substrate (Thr) #status predicted
F; 132/Rinding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
F; 172/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
F; 172/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Pusarium sporotrichioides
C; Date: 13-Uun-1995 #sequence_revision 14-Jul-1995 #text_change 19-Jan-2001
C; Accession: JT0686; PN0166; JT0702
R; Chow, L.P.: Ueno, Y.; Tsugita, A.
submitted to JIPID, June 1995
A; Description: Amino acid sequence of peptidyl-prolyl isomerase a from Fusarium sporo
A; Reference number: JT0686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 1-179 <CHO>
R;Fukaaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchl, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: PN0160
A;Accession: PN0166
A;Molecule PN0166
A;Molecule FURS
B;Chow, L.P.; Kamo, M.; Ueno, Y.; Tsugita, A.
submitted to JIPID, August 1995
A;Description: Amino acid sequence of peptidyl-prolyl Isomerase a of Fusarium sporotr A;Reference number: JT0702
A;Accession: JT0702
   A; Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds C; Superfamily: peptidylprolyl isomerase; cyclophilin homology C; Keywords: cis-trans-isomerase; cyclosporin A binding; T-cell F; 3-164/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptidylprolyl isomerase (EC 5.2.1.8) a, cytosolic – fungus (Fusarium sporotrichiolde
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                                                                                                                                                                                                                  DB 1;
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0; Mismatches
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Pred. No.
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Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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CSNCM
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A; Residues: 2-21 < KRU>
A; Residues: 2-21 < KRU>
A; Residues: 2-21 < KRU>
A; Experimental source: nuclear cyclophilin of H4-7 cells
C; Genetics:
A; Gene: CypA
C; Function:
A; Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
C; Keywords: cis-trans-isomerase; cyclophilin homology
F;3-164/Domain: cyclophilin homology < CYP>
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A; Molecule type: mRNA
A; Residues: 100-148, WARPARRSPSPTVGNSNFFDLRAFYPSNH', 'SFCSSGEHPHPICSQYPVISALTEVLWVP', 'YFH
A; Cross-references: EMBL:M25637
A; Note: this sequence was corrected by A58859
R; Meyuhas, O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptidylprolyl isomerase (EC 5.2.1.8) A - rat
N;Alternate names: 13.3K protein [misidentification]; cyclophilin A; cyclosporin A-bindi
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1992 #sequence_transportation 31-Mar-1992 #text_change 04-Feb-2000
C;Accession: A29819; A60036; A15632; A15632;
B;Danielson, P.E.; Forss-Petter, S.; Brow, M.A.; Calavetta, L.; Douglass, J.; Milner, R.
DNA 7, 261-267, 1988
A;Title: plBl5: A cDNA clone of the rat mRNA encoding cyclophilin.
A;Reference number: A29819; MUID:88283345
A;Accession: A29819
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A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-164 <LAD>
A;Residues: 1-164 <LAD>
A;Experimental source: brain
R;Theodor, L.; Peleg, D.; Meguhas, O.
Biochim. Biophys. Acta 826, 137-146, 1985
A;Title: P31, a mammalian housekeeping protein encoded by a multigene family contain A;Reference number: A15632: MUID:86026347
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                                                                                                                                                      in macrophages
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A; Residues: 1-164 cADA7.
A; Residues: 1-164 cADA7.
A; Cross-references: GB: M19533; NID: g203701; PIDN: AAA1009.1; PID: g203702
R; Lad, R.P.; Smith, M.A.; Hilt, D.C.
R; Lad, R.P.; Smith, M.A.; Hilt, D.C.
Brian, Ress. Mol. Brain Ress. 9, 233-244, 1991
A; Title: Molecular cloning and regional distribution of rat brain cycloph A; Reference number: A60036; MUID: 91232390
ö
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Pred. No. 2.4;
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A;Molecule type: mRNA
A;Residues: 1-164 <MEY>
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Best Local Similarity 77.8%;
Matches 7; Conservative
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31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

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C;Accession: A41581
R;Bergsma, D.J.; Eder, C.; Gross, M.; Kersten, H.; $ylvester, D.; Appelbaum, E.; Cusi
t, W.P.; Bossard, M.J.; Brandt, M.; Levy, M.A.
J. Biol. Chem. 266, 22204-23214, 1991
A;Title: The cyclophilin multigene family of peptidyl-prolyl isomerases. Characteriza A;Reference number: A41581; MUID:92078192
                                                                                                                                                                        peptidylprolyl isomerase (EC 5.2.1.8) 3 precursor - human
N;Contains: cyclophilin
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #fext_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M80254; NID:g181273; PIDN:AAA58434.1; PID:g181274 (S.Superfamily: peptidy!prolyl isomerase: cyclophilin.homology C;Reywords: cis-trans-isomerase: cyclosporin A binding; mitochondrion F:45-206/Domain: cyclophilin homology <CYP>
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Pred. No. 4.6;
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Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-207 <BER>
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A; Crooss-references: RRBL:X17692; NID:92998; PIDN:CAA35681.1; PID:9295926
C; Comment: The mature cytosolic and mitochondrial forms are identical in sequence, although in al residue.
C; Function:
A; Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
C; Keywords: alternative intitators: alternative splicing; cis-trans-isomerase; cyclospor
C; Keywords: alternative intitators: alternative splicing; cis-trans-isomerase; cyclospor
F; 1-180/Product: peptidylprolyl isomerase mitochondrial form precursor #status predicted
F; 14-237/Domain: propeptide (mitochondrion) #status predicted CT F; 44-237/Domain: propeptide (mitochondrion) #status predicted CT F; 44-237/Domain: propeptide (mitochondrion) #status experimental 
F; 44-2180/Product: peptidylprolyl isomerase cytosolic form precursor #status predicted CT F; 45-180/Product: peptidylprolyl isomerase, mitochondrial #status experimental 
F; 45-180/Product: peptidylprolyl isomerase, mitochondrial #status experimental 
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S68767
peptidylprolyl isomerase (EC 5.2.1.8) - rat (fragments)
N;Alternate names: cyclophilin
C;Species: Rattus norvegicus (Norway rat)
C;Accession: S68767
R;Tanveer, A.; Virjl, S.; Andreeva, L.; Totty, N.F.; Hsuan, J.J.; Ward, J.M.; Crompton, R;Tanveer, A.; Virjl, S.; Andreeva, L.; Totty, N.F.; Hsuan, J.J.; Ward, J.M.; Crompton, R;Teference number: S68767; MUID:96248435
A;Rotession: S68767
A;Rotession: S68767
A;Rotession: S68767
A;Rotession: S68767
A;Rotession: S68767
C;Superimental source: liver
C;Superimental source: liver
C;Superimental source: liver
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Reywords: cis-trans-isomerase; cyclosporin A binding; mitochondrion
C: Accession: B30809; A30809; S07585

R: Tropschug, M.; Nicholson, D.W.; Hartl, F.U.; Koehler, H.; Pfanner, N.; Wachter, E.; Ne Tropschug, M.; Nicholson, D.W.; Hartl, F.U.; Koehler, H.; Pfanner, N.; Wachter, E.; Ne A: Title: Cyclosporin A-binding protein (cyclophilin) of Neurospora crassa. One gene code A: Reference number: A92671; MUID: 89008293

A: Accession: B30809

A: Accession: A30809

A: Accession: A4-223

A:
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A;Reference number: S07585; MUID:90174923
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CYPB_BOVIN
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7.7 331 1 7.7 331 1 7.7 331 1 7.7 331 1 7.7 396 1 7.7 1085 1 7.7 185 1 7.7 1	STANDARD;	el. 20, Creat el. 20, Last el. 40, Last CIS-TRANS I	(Human). tazoa; Chordat. heria; Primate 06;	N.A., AND SEQ 14; PubMed=20 dowsky L.D.,	llin B: a sec se with a sig id. Sci. U.S	1.A. 3: PubMed=20 er B., Delma reuil J., St. Movva N.R.; ed cyclophil 266:10735-10	108 FROM N.A. 17: PubMed=17: Godl 18s J.R., Godl 1: reticulum=si	76 AND 151-1: 3; PubMed=12: van Damme J J.; of 145 proteie of normal is of 13:960-969(CCATION. 448; PubMed-153094 838e KH., Caroni 1 is retained intricolocalizes with t	GRAPHY (1.85 5; PubMed=81 n J., Walkin
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	RESULT 1 CYPB_HUMAN ID CYPB H		500003	RA RA B	R R T F F	R R R R R R R R R R R R R R R R R R R			RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	

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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-MAR-1992 (Rel. 21, Last sequence update)
15-JUL-1999 (Rel. 28, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-SI).
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"X-ray structure of a cyclophilin B/cyclosporin complex: comparison with cyclophilin A and delineation of its calcineurin-binding
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                   Proc. Natl. Acad. Sci. U.S.A. 91:5183-5186(1994).

-1- FUNCTION: PDIASES ACCELERATE THE FOLDING OF PROTEINS.
-1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
-1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULM LUMEN.
-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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Pfam: PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMASE.
PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE: PS50072; CSA_PPIASE_2; 1.
Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family; 3D-structure.
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An endoplasmic reticulum-specific cyclophilin.";
MOI. Cell. Biol. 11:3484-3491(1991).
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EMBL; M63573; AAA36601.1; ALT_INIT.
EMBL; M60457; AAA35733.1; -.
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PIR; A40515; A40515.
PDB; ICYN; 29-JAN-96.
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                                                                                                                                                                                                                                          SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     œ.
                                  ø
                         Murine cyclophilin-SI: a variant peptidyl-prolyl isomerase with a putative signal sequence expressed in differentiating F9 cells."; Blochim. Biophys. Acta 1129:13-22 (1991).
-!- FUNCTION: PETASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- ENZYME REGULATION: CYCLOSPORINA (CSA) INHIBITS CYPB.
-!- SUBCELLULAR LOCATION: BNDOPLASMIC RETICULUM LUMEN (BY SIMILARI).
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90300692; PubMed-2194066;
Iwai N., Inagami T.;
"Molecular cloning of a complementary DNA to rat cyclophilin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PREVENT SECRETION FROM ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.

SIGNAL 1 25 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
Schroeter H., Multhaup G., Nordheim A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY),
4BBDF5AE40BAD3A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro: IPR00130; CSA_pplase.
Pfam: PF00160; pro_isomerase; 1.
PRINTS: PR00153; CSAPPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92112948; PubMed=1530944; Arber S., Krause K.-H., Caroni P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kidney Int. 37:1460-1465(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M60456; AAA37498.1; -.
EMBL; X58990; CAA41736.1; -.
PIR; B39722; B39722.
PIR: S21835; S21835.
HSSP; P23284; ICYN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS TO C-TERMINUS.
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208
208
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GFGYKNSKF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 GFGYKNSKF
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208 AA;
                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                 77 GFGYKDSKF 85
                                                                                                                                                                                                                                                                                      1 GFGYKNSKF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6210;
                                                                                                              P23284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Echinococcus
                                                                                                                                                                                                                                                                                                                                                     CYPH_ECHGR
P14088;
                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                           CYPH_ECHGR
                                                                                                                                                                                                                                                                    Matches
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                        "S-cyclophilin is retained intracellularly via a unique COOH-terminal sequence and colocalizes with the calcium storage protein calreticulin.";
                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
EPPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
SIGNAL
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0
                                                                                                                                                                                                                             100.0%; Score 51; DB 1; Length 208; 100.0%; Pred. No. 0.02;
                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carrello A., Mark P.J., House A.K., Ratajczak T.;
Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                 PREVENT SECRETION FROM ER (BY SIMILARITY).
76D12AC3427FEF32 CRC64;
                                                                                                                                                                                                                                      Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                208 AA.
                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                               Interpro; IPR002130; CSA_PPIASe.
Pfam; PF00160; pro_isomerase; 1.
PRNUTS; PR00153; CSAPPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain;
MEDLINE-94283623; PubMed-8013656;
                                                                                                                                                                                                  208 AA; 23025 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to cyclophilin-A.";
FEBS Lett. 347:31-36(1994).
                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                               25
208
208
                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 26-45.
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77 GFGYKNSKF 85
                                                                                                                                                                                                                                                                1 GFGYKNSKF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE * Uterus;
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P80311:
                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                        CHAIN
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01-NOV-1995 (Rel. 32, Last Sequence (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) (FRAGMENT).
Echinococcus granulosus.
Eukaryota, Metazoa, Platyhelminthes; Turbellarian Platyhelminths;
Rhaboditophora, Eulecithophora, Revertospermata; Mediofusata;
Neodermata; Cestoda; Eucestoda; Cyclophyllidua; Taeniidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen of Echinococcus granulosus.";
Mol. Blochem. Parasitol. 36:287-290(1989).
-! FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-! CAPALYTIC ACTIVITY: CIS-TRANG ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-! ENXYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
-! SUBCELLULAR LOCATION: CYTOPLASMIC.
-! SIMILARITY: BELONGS TO THE CYCLOPHILIN'TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-90014983; PubMed-2677720;
Lightowlers M.W., Haralambous A., Rickard M.D.;
"Amino acid sequence homology between cyclophilin and a cDNA-cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B. PREVENT SECRETION FROM ER. K -> G (IN REF. 3): 0097C88289AF6276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
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SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 1; Length 208; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                        Interpro; IPR002130; CSA_pplase.
Pfam; PF00160; pro_isomerase; 1.
PRNUTS; PR00153; CSAPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1; IPROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
208 PE
208 PE
30 K
22701 MW;
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                                                                                                                                                                                                                                                                                EMBL; D14073; BAA03158.1; -.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                  CYPC_HUMAN
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                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
                                                                                                                                                                                                                                                                                                                                     ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- TISSUE SPECIFICITY: UBIQUITOUS.
-i- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biattella germanica (German cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blattellidae; Blattellinae; Blattella.
NGBI_TaxID=6973;
                                                                                                                                                                                                                                                                                       88.2%; Score 45; DB 1; Length 161;
88.9%; Pred. No. 0.19;
iive 0; Mismatches 1; Indels
                                                                                                                                                                             Cyclosporin; Isomerase; Rotamase; Multigene family.
NON_TER 1
SEQUENCE 161 AA; 17223 MW; 72661E2F4FEF466F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Isomerase; Rotamase.
164 AA; 17935 MW; A5E25B574DFCDC99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 AA
                                                                 HSSP; P05092; 3CYS.
InterPro; IPR002130; CSA_PPIase.
Jefan; PP00160; pro_isomerase; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; P550072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-96096751; Pubmed-8529654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X87418; CAA60869.1; -. HSSP; P05092; 1AWV.
                        EMBL; J04664; AAA29058.1;
PIR; A45000; A45000.
                                                                                                                                                                                                                                                                                       Ouery Match 88.2
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                        42 GFGYKGSKF 50
                                                                                                                                                                                                                                                                                                                                                                             1 GFGYKNSKF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclosporin;
SEQUENCE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYPH_BLAGE
P54985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
CYPHENAGE
CYPHENAGE
DT 01-0CT-1
DT 01-0CT-1
DT 01-0CT-1
DT 01-0CT-1
DE PERTON
CON BLALKE
C
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DB 1; Length 164;

82.4%; Score 42;

Query Match

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                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.
-1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94304813: PubMed-8031755; Schmitz R., Wehrli S., Mikol V., Schmitz R., Wehrli S., Mikol V., Schmitz R., Wehrli S., Mikol V., Schmitz R., Weyshill S., Ordon V., Movey N.R., West G., Quesaniaux V.F., Movey N.R., Issue distribution, and determination of binding specificity for cyclosporins."; Biochemistry 33:8218-8224(1994).

--- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTIENS.
--- FUNCTION: PRIASES ACCELERATE THE FOLDING OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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Pred, No. 0.88;
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclosporin; Isomerase; Rotamase; Multigene family. SEQUENCE 212 AA; 22763 MW; 6F3DB547A2AE581B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 AA
                                                                                                                                                                                                                                                                       212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
Pred. No. 0.7; Mismatches
                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPLES IPPROBLEM CSA_PPIASE.
Pfam: PF00160; pro_isomerase: 1.
PRINTS: PR00155; CSAPPISHRASE.
PROSITE: PS00170; CSA_PPIASE_1; IPROSITE; PS0072; CSA_PPIASE_1; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 21, Created)
(Rel. 21, Last seque
(Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.48;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; S71018; AAB31350.1; -. HSSP; P05092; 2RMC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 77.8 es 7; Conservative
                            7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                             |||||| |:|
45 GFGYKGSRF 53
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                                                                              1 GFGYKNSKF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 123842; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
CYPE_CHICK
ID CYPB_CHICK
AC P24367;
DT 01-MAR-1992 (
DT 15-JUL-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPIC OR CYPC.
                                                                                                                                                                                                                                                                       CYPC_HUMAN
P45877;
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us-09-720-469-3.rsp

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RAHARA BARAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οχ
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01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIOYL-PROLYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLUIAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE) (RYGNAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
Gallus gallus (Chicken).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-91250364; PubMed-2040593;
Caroni P., Rothenfluh A., McGlynn E., Schneider C.;
"S-cyclophilin. New member of the cyclophilin family associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                         Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Verrebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PREVENT SECRETION FROM ER (BY SIMILARITY).

D9C0C2E528E25B59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P23284; ICYN.
InterPro: IPR002130; CSA_PPIase.
Pfam: PF00160; pro_lsomerase; 1.
PR01TS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-90174932; PubMed-2408007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22413 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M63553; AAA49064.1; -. PIR; A40516; A40516.
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Best Local Similarity 77.8
Matches 7; Conservative
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207
207
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76 GFGFKGSKF 84
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                                                                                                                                                    NCBI_TaxID-9031;
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P14851;
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CYPH_CRILO
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN) (SP18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
          Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBL_raxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.4%; Score 40; DB 1; Length 163; 77.8%; Pred. No. 1.6; 1.ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 AA; 17768 MW; 02D44F71B8F87A1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclosporin; Isomerase; Rotamase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-19; 21-27 AND 76-84.
                                                                                                                                                                                                                                                                                                                                         HSSP, P05092; 3CYS.
InterPro, IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                            EMBL; X17105; CAA34961.1; -.
Bergsma D.J., Sylvester D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                              PIR; S07597; CSHYAC.
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 GFGYKGSSF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFGYKNSKF 9
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by a multigene family

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CYPH_NEUCR
P10255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INIT_MET
SEQUENCE
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CYPH_NEUCR
      NAMES OF A PROPERTY OF A PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
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P10111; P18303;
01-MAR-1989 (Rel. 10, Created)
01-NAR-1989 (Rel. 10, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAWASE)
(CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN) (P31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE. SUBCELLULAR LOCATION: CYTOPLESMIC. SIBILIARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.4%; Score 40; DB 1; Length 163; 77.8%; Pred. No. 1.6; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lad R.P., Smith M.A., Hilt D.C.; "Molecular cloning and regional distribution of rat brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRV -> TXP (IN REF, 2).
: AC724D44DBBF4840 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclosporin; Isomerase; Rotamase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brain Res. Mol. Brain Res. 9:239-244(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
MEDLINE-88283345; PubMed-3293952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; $10327; CSMSA.
HSSP; P05092; 3CYS.
SWISS-2DPAGE; P17742; MOUSE.
MGD; MGI:97749; Ppla.
InterPro; IPR002130; CSA_PPIASE.
Pfam; PP00160; pro_1somerase; 1.
PROSITE; PS00179; CSA_PPIASE.;
PROSITE; PS00170; CSA_PPIASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
MEDLINE-91232390; PubMed-1851525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-86026347; PubMed-2996604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theodor L., Peleg D., Meyuhas O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 AA; 17840 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X52803; CAA36989.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 GFGYKGSSF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GFGYKNSKF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SABRA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cyclophilin.
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CONFLICT
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                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) (CPH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89008293; PubMed-2971658;
Tropschug M., Nicholson D.W., Hartl F.-U., Kohler H., Pfanner N.,
Wachter E., Neupert W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
NCBL_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 1; Length 163;
Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 AA; 17743 MW; DD16D1C9B0474414 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclosporin; Isomerase; Rotamase; Multigene family.
"P31, a mammalian housekeeping protein encoded containing a high proportion of pseudogenes."; Blochim. Biophys. Acta 826:137-146(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002130; CSA_PPIBASe.
Pfam; PF00160; pro_isomerase; 1.
PRNINTS; PR00153; CSAPPISARASE.
PROSITE; PS00170; CSA_PPIBASE_1; IPROSITE; PS50072; CSA_PPIBASE_2; 1.
                                                                                                                                                   MEDLINE-92287042; PubMed-1599421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M19533; AAA41009.1; -. EMBL; M25637; AAB59719.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 77...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A15632; CSRT31.
PIR; A29819; CSRTA.
HSSP; P05092; 3CYS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurospora crassa.
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                                                                                                SEQUENCE OF 1-28 TISSUE-Liver;
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86 GFGYKGSTF 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
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                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
                                                                                Eukaryota: Metazzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
 "Cyclosporin A-binding protein (cyclophilin) of Neurospora crassa. One gene codes for both the cytosolic and mitochondrial forms."; J. Biol. Chem. 263:14433-14440(1988).
                                                                     Nucleotide sequence of the gene coding for cyclophilin/peptidyl-
                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclosporin; Isomerase; Rotamase; Mitochondrion; Transit peptide; Alternative initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EPPTIDYL-PROLYL CIST-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR (EC. 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPIASE, MITOCHONDRIAL ISOFORM.
PPIASE, CYTOSOLIC ISOFORM.
D494AB77F9768AEO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.4%; Score 40; DB 1; Length 223; 77.8%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                PIR, A30809; CSNCC.
PIR, B30809; CSNCM.
HSSP, P06092; 3CYS.
Interpro: IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                   MEDLINE-90174923; PubMed-2137907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 44 F
223 AA; 24064 MW;
                                                                                                                                                                                                                                                                                                 EMBL; J03963; AAA33584.1; -.
EMBL; X17692; CAA35681.1; -.
EMBL; X17692; CAA35682.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 77.8.
77.67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
"Cyclosporin A-binding
                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 GFGYKGSSF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFGYKNSKF 9
                                                               Tropschuq M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYPM_RAT P29117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U68544; AAB08453.1; -
HSSP; POSO92; 3C3722
HSSP; POSO92; 3C3722
HSSP; DOSO92; 3C372
InterPro: IPRO130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRO151E; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_2; 1.
PROSITE; PS00170; CSA_PPIASE_2; 1.
Transit peptide.

29 MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
BEDLINE=92078192: PubMed=1744118;
Bergsma D.J., Edder C., Gross M., Kersten H., Sylvester D.,
Appelbaum E., Cusimano D., Livi G.P., McLauglin M.M., Kasyan K.,
Porter T.G., Silverman C., Dunnington D., Hand A., Prichett W.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDYL-PROLYL CIS-TRANS ISOMERASE MISSING (IN A MINOR FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR
(EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 1; Length 206;
Pred, No. 3;
STRAIN=WISTAR; TISSUB=Skeletal muscle;
Price N.T., Woodfield K.Y., Halestrap A.P.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S -> R.
C -> A (IN REF. 2).
69048482631B9FAD CRC64;
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206 P.
39 M.
31 S.
30 C.
21810 MW,
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ilarity 77.8%;
Conservative (
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Matches 7; Conserv
                                                                                 SEQUENCE OF 30-58
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1610 163
1669 168
1728 174
1785 180
2013 243
2310 243
2310 243
2912 304
3063 322
77 78
3224 AA;
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1419
1483
1547
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SEQUENCE
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ZN_FING
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ZN_FING
ZN_FING
ZN_FING
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                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 40, Last annotation update)
RAN-BINDING PROTEIN 2 (RANBP2) (NUCLEAR PORE COMPLEX PROTEIN NUP358)
(NUCLEOPORIN NUP358) (358 KDA NUCLEOPORIN) (P270).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95294031; PubMed=7775481; Wu J., Matunis M.J., Kraemer D., Blobel G., Coutavas E.; Wu J., Matunis M.J., Kraemer D., Blobel G., Coutavas E.; Nup358, a cytoplasmically exposed nucleoporin with peptide repeats, Ran-GTP binding sites, zinc fingers, a cyclophilin A homologous domain, and a leucine-rich region."; J. Blol. Chem. 270:14209-14213(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclosporin; Isomerase; Rotamase; Multigene family; Mitochondrion;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 MITOCHONDRION (POTENTIAL).
207 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
22040 MW; D7C76F1D4049F16A CRC64;
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MEDLINE-95327194; PubMed-7603572;
Yokoyama N., Hayashi N., Seki T., Nishii K., Hayashida T.,
Kuma K.I., Miyata T., Fukui M., Nishimoto T., Pante N., Aebi U.;
"A giant nucleopore protein that binds Ran/TC4.";
Nature 376:184-188(1995).
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                                                                                                                                                              -! - SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY
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Pfam: PF00160; pro_isomerase: 1.
PROSITE: PR00153; CSAPPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1: 1.
PROSITE; PS00772; CSA_PPIASE_2: 1.
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PIR; A41581; A41581.
HSSP; P05092; 3CYS.
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Best Local Similarity 77.8
Matches 7; Conservative
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MIM; 604486;
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Search completed: January 15, 2002, 13:14:59 Job time: 655 sec

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O02614 leishmania
Q99kr7 mus musculu
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09xzz5 lumbricus r
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O9r137 mus musculu
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09czk9 mus musculu
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(without alignments)
16.696 Million cell updates/sec
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O01490 orpinomyces
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Q25093 hirudo medi
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries

    protein search, using sw model

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sp_mammal:*
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Q9ass6 arabidopsis
Q9eru9 mus musculu
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SEQUENCE FROW N.A.

SEQUENCE FROW N.A.;

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TAYLOPHILIN B.";

"Cyclophilin B.";

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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U-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN B (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 AA
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Q51011
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Gaps

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100.0%; Score 51; DB 11; Length 208; 100.0%; Pred. No. 0.083;

Mismatches

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9; Conservative

GEGYKNSKF 85 1 GFGYKNSKF 9

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Best Local Similarity Matches 9; Conserv

Query Match

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Query Match 100.

Best Local Similarity 100.

Matches 9; Conservative
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Matches 8; Conservative
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71 GYGYKNSKF 79
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REQUENCE TO FUNGED-11217851;

REDINE-21085660; PubMed-11217851;

RA ALZAWA T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA ALZAWA T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA ALZAWA T., Caxaaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

RA Galto T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Yaamaaka I.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kehl P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Harchjonni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Myashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RA Functional annotation of a full-length mouse cDNA collection.";

RE Nature 4095865-690(2001).

RE Nature 4095865-690(2001).
                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0
                                                                                                                                                                                                                                                                                                                                   100.0%; Score 51; DB 4; Length 216; 100.0%; Pred. No. 0.086;
                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                  Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases EMBL; BC001125; AAH01125.1; -.
                                                                                                                                                                                                                                                                                            216 AA; 23742 MW; 2D0410A07AA9E420 CRC64;
                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                     216 AA
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, PEPTIDYLPROLYL ISOMERASE B.
                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-SKIN, AND MELANOMA;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                     PRELIMINARY;
                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-10090;
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                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                Isomerase.
                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                    Q9BVK5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9DCY1
                          RESULT
09BVK5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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ACHON HILL STAZESSON FURNED-T/00090;

RT A Cyclophilin from the polycentric anaerobic rumen fungus Orpthomyces

RT Proc. Natl. Acad. Sci. U. S. A. 9212587-2591(1995).

RL PROC. Natl. Acad. Sci. U. S. A. 9212587-2591(1995).

CI - CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROPIENS.

CI - CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

PEPPIDE BONDS IN OLIGOREPHIDES.

CI - ENEXTME REGULATION: CYCLOSPORIN A (CSA) INHEBITS CYPB.

CI - SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

EMBL. U1790: AAD04195.1;

RSSP; P23284; ICYN.

INTEFPC: IPR00130; CSA_PPIASE.

RRICH PROSITE: PS00170; CSA_PPIASE.

RRINTS; PR00153; CSA_PPIASE.

RW ISOMERSES: REGULANDES.

RRINTS; PS00170; CSA_PPIASE.

RW ISOMERSES: REGULANDES.

RW ISOMERSES: REGULANDES.

RRINTS; PS00170; CSA_PPIASE.

RW ISOMERSES: REGULANDES.

RW 
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(CYCLOPHILIN B) (ROTAMASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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PREVENT SECRETION FROM ER
SIMILARITY).
A5748C94305B8BE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Orpinomyces sp. PC-2.
Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
Neocallimasticaceae; Orpinomyces.
NCBI_TaxID=50059;
Pfam: PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPISMASE.
PROSITE; PS50072; CSA_PPIASE_2; 1.
SEQUENCE 216 AA; 23713 MW; CE9DAD1544AE72FE CRC64;
                                                                                                                                                                                                                                                             100.0%; Score 51; DB 11; 100.0%; Pred. No. 0.086;
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Pred. No. 0.29;
1; Mismatches (
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MEDLINE-95223986; Pubmed-7708690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q98UE5;
01-JUN-2001 (TrEMBLrel. 17, Created)
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88,9%;
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PEDURNCE.
MEDLINE-92031730; PubMed-1932134;
MEDLINE-92031730; PubMed-1932134;
MEDLINE-92031730; PubMed-1932134;
Meditor T.R., Tabatabal L., Bruns K., Hamilton R.T., Nilsen-Hamilton M.;
"Basic fibroblast growth factor induces 373 fibroblasts to synthesize and secrete a cyclophilin-like protein and beta 2-microglobulin.";
Blochlin Blochlin Blophys. Acra 1095:145-152(1991).
InterPro: IPR00130; CSA_PPIAse.
Pfam; PF00160; pro_isomerase; 1.
SEQUENCE 17 AA; 1785 WW; 11276657FEB240D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colgan J.D., Asmal M., Luban J.;
"Haploinsufficient growth defects, increased Th2 cytokine production and cyclosporine resistance in mice lacking CYPA.";
submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF171073; AAD50996.1;
HSSP: P05092; 2CPL.
                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                           01-MMY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SUPERINDUCIBLE PROTEIN 24, SIP24*CYCLOPHILIN HOMOLOG, PEAK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.4%; Score.40; DB 11; Length 17; ilarity 77.8%; Pred. No. 0.65; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CB53F70E1092889C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
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Pred. No. 1.5;
0; Mismatches 2
                                                                           17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 AA.
                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD: MGI:97749; Ppia.
InterPro; IPR002130; CSA_PPIase.
Pfam: PF00160; pro_isomerase; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 AA; 4324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 77.8
Matches 7; Conservative
                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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Best Local Similarity
Tr Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 GFGYKGSSF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GFGYKGSSF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GFGYKNSKF
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                                                                         940060
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                          "Isolation of genes involved in intestinal remodeling during anuran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lumbricus rubellus (Humus earthworm).
Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
Lumbricina; Lumbricidae; Lumbricus.
NCBI_TaxID=35632;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERARE B (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi; Amphibia; Batrachia: Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Sturzenbaum S.R., Morgan A.J., Kille P.;
"isolated from earthworms exposed to Cd-supplemented artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 13; Length 104;
Pred. No. 1.8;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.4%; Score 41; DB 5; Length 164; 77.8%; Pred. No. 4.4; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                              Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF170328; AAK11503.1;
                                                                                                                                                                                                                                                                                                                                                104 AA; 11350 MW; 8F6AD1CD1C2FB3E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 AA; 17599 MW; B30D22D660966AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN A (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam: PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ238310; CAB41016.1; -. HSSP; P05092; 1CWL. InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                             82.48;
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                  SEQUENCE FROM N.A.
Amano T., Yoshizato K.;
                                                                                                                            Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isomerase; Rotamase.
SEQUENCE 164 AA;
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Best Local Similarity
Matches 7; Conserv
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77 GYGYKGSKF 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GFGYKNSKF 9
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                                                                                                                                                                                                                                                metamorphosis.
                                                                                                                                                                                                                                                                                                               somerase.
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SEQUENCE
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Query Match

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Q9X225 9

RESULT Q9XZZ5

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Gaps

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Isomerase; Rotamase.
                                                                                           Isomerase; Rotamase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      24 GFGYKGSSF 32
                                                                                                                                                                                                                                             1 GFGYKNSKF 9
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                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  Q9CWJ5;
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                                                                                                                                                                                                                                                                                                                                          RESULT 11
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Korneev S., Blackshaw S.E., Kalser K., Davies J.A.;

Found libraries from identified neurons.";

Proc. R. Soc. Lond., B. Biol. Sci. 263:57-62(1996).

FOLDING OF PROTEINS (BY SIMILARITY).

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FOLDING SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.

EMBL. U36797: AABOLS31.1; -.

#SSP: P05092; 2CPL.
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Annellda; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
NCBI_TaxID=6421;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 AA; 7841 MW; 472374C1287ACEC9 CRC64;
                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN (FRAGMENT).
Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN-A (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.4%; Score 40; DB 11;
77.8%; Pred. No. 2.8;
tive 0; Mismatches 2;
                                                     70 AA.
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                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00160; pro_isomerase: 1. PRINTS; PR00153; CSAPPISMRASE. PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96165729; PubMed-8587897;
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                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isomerase; Rotamase.
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Best Local Similarity
Matches 7; Conserv
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24 GFGYKGSSF 32
                                                                                                                                                                                                                                               NCBI_TaxID=10036;
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SEQUENCE
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                                                     Q9ERB9
                                                                         09ERB9
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CETRAINCESTBL/GBT. TISSUB-EMBRYONIC STEM CELLS;

RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Radota K., Matsuk H., Ashburner M., Batalov S., Casavant T., Radota K., Matsuk H., Ashburner M., Batalov S., Casavant T., Radota K., Matsuk S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Rohil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Saki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Baka Sakai K., Okido T., Futuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Auyons P., Matchionni L., Mashima J., Manazarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Satorch K.-F., Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mashiaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hangashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.
EMBL; AKOLO649; BABZ7089.1; -.
MGD; MGI:97749; Ppia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                Length 143;
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                                                                                                                                                                                                        143 AA; 15398 MW; 64FFD82018480A6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYLPROLYL ISOMERASE A.
                                                                                                                                                                                                                                                                                                                    l; DB 5;
1, 5.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 AA
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                                                                                                                                                                                                                                                                                                                       Score 40;
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Interpro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRNUTS; PR00153; CSAPPISMASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002130; CSA_PPIase
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Best Local Similarity 77.8%;
Matches 7; Conservative (
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Length 164;

DB 11;

78.4%; Score 40;

Q9CZK9; **09CZK9**

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Mismatches
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                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
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PRINTS; PR00153; CSAPPISMRASE.
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InterPro; IPR002130; CSA_PPIase
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
            PRELIMINARY;
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                                                                                                                                                 (P34791) (FRAGMENT).
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Arakawa T., Hara A., Fibata K., Yoshino M., Itch M., Ishli Y.,
Arakawa T., Hara A., Fibata K., Konoo H., Adachi J., Fukuda S.,
Alazawa K., Izawa M., Nishi K., Kiyosawa T., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Raukawa T., Saito R.,
A Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsud T., Gassic. T., Mikaldo I., Pesole G., Quackenbush J.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Lyons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodtiguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Namate 409:865-690(2001).
A Hayashizaki Y.;
Pructional annotation of a full-length mouse cDNA collection.";
A Purch of PROTEINS BY SIMILARITY).
C -- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
C ACPALITY CACTIVITY: CIS-TRANS ISOMERASES ACCELERATE THE
C C -- PEPPITOF HONDS IN OLICORDEMINE INDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                               ;
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                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 AA; 18314 MW; 399BC62857BDA9EB CRC64;
                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                          2;
                                                                                                                                                                                                                                    167 AA
  77.8%; Pred. No. 6.7;
                             Mismatches
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MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: CIS-TRANS PEPTIDE BONDS IN OLIGOPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPTASE_1; 1.
PROSITE; PS50072; CSA_PPTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANS ISOMERASE FAMILY.
EMBL, **AROL2491; BAB38276.1; -.
MGD; MGI:97749; Ppia.
InterPro: IPR002130; CSA_PPIase.
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                                                                                                                                                                                                                                                                      01-JUN-2001 (TremBLrel. 17, 01-JUN-2001 (TremBLrel, 17, 01-JUN-2001 (TremBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                  PEPTIDYLPROLYL ISOMERASE A.
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Matches 7; Conservative
                     7; Conservative
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Best Local Similarity
Matches 7; Conserv
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                                                                                              45 GFGYKGSSF 53
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48 GFGYKGSSF 56
                                                                 1 GFGYKNSKF 9
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Query Match

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13

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Gaps
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"Isolation of a cDNA sequence encoding a peptidyl-prolyl cis-trans isomerase from Periplaneta americana antennae.";

Submitted (JAN-1998) to the EMBL/Genank/DDBJ databases.

-! FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).

-! CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

-! SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO ARABIDOPSIS THALIANA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
                                                                                                                                                                                                               SEQUENCE FROM N.A.
Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M.,
Chen C.-S., Shaw J.-F.;
Oryza sativa PAC P0036D10 genomics sequence, complete sequence.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC073405; AAG03106.1; -
                                                                            Oryza sativa (Rice).
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROCKI CIS-TRANS ISOMERASE (FRAGENT).
Periplaneta americana (American cockroach).
Periplaneta, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meoptera; Orthropteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 10; Length 173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 173 AA; 19158 MW; 28EADE80F4625EB9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (FRAGMENT).
LM12.959.
Leishmania major.
Leishmania Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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Query Match 76.5%; Score 39; DB 5; Length 78; Best Local Similarity 77.8%; Pred. No. 4.7; Matches 7; Conservative 0; Mismatches 2; Indels
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147 AA; 15620 MW; 9074B7BC8980B4EA CRC64;
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Best Local Similarity 77.8
Matches 7; Conservative
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Search completed: January 15, 2002, 13:16:25 Job time: 656 sec

30 GFGYANSPF 38

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January 15, 2002, 13:05:27 ; Search time 81.32 Seconds (without alignments) 10.020 Million cell updates/sec
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| SIDS8/gradata/geneseq/geneseqp/AA1980.DAT:
| SIDS8/gradata/geneseq/geneseqp/AA1991.DAT:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	Description	Human ovelonbilin	Human secreted oro	Human cyclophilin	Himan cyclohilin	Himan Capter assoc	Caenorhabditis ele	D. discoldena ovol	Human prostate can	Human cyclonhilin	Arahidonsis thalia	Arabidopsis thalia	
SUMMARIES		ID	AAY69924	AAG00090	AAB73302	AAB73301	AAB43878	AAB49141	AAW80784	AAB56701	AAU01197	AAG16463	AAG05073
		DB	21	21	22	22	21	22	19	21	22	21	21
		Query Match Length DB ID	11	166	211	216	291	171	180	183	207	252	254
	æ	Query Match	100.0	100.0	100.0	100.0	100.0	80.0	80.0	80.0	80.0	80.0	80.0
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		Result No.	7	8	m	₹	'n	9	7	80	σ	10	11

Tumour antigen peptides derived from cyclophilin B for treatment and diagnosis of tumours \cdot

(SUMU) SUMITOMO PHARM CO LTD.

WPI; 2000-116932/10. Gomi S;

Itoh K,

99WO-JP03360, 98JP-0178449.

24-JUN-1999; 25-JUN-1998;

29-DEC-1999

Claim 4; Page 50; 64pp; Japanese.

4	80.0	254	21	AAG16462	thali
4	80.0	259	21	AAG05072	Arabidopsis thalia
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4	8	218	21	AAG29379	or.
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4	9	212	14	AAR32353	Cyclophilin C. Mu
4	S.	108	21	AAG03830	ced p
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4	'n.	114	22	AAB64736	
4	υ.	145	12	AAR10763	peptid
4.	ش ر	145	16	AAR72917	Porcine peptidyl p
4.	٠ د د	145	9	AAR72961	Porcine peptidyl p
4.	٠ د	163	75	AAR13726	Bovine cyclophilin
4.	٠. د	164	10	AAP90431	Cyclophilin. Home
4.	٠ د د	165	6	AAW56028	Calcineurin protei
4.	'n.	165	21	AAG03831	Human secreted pro
4.	٠ ، ،	165	7.7	AAU01195	Human cyclophilin
♥ -	ر. د	527	22	AAB49136	
4	'n	527	22	AAB49137	tis cyclo
4	m	09	22	AAB59530	secreted
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4	m 1	141	19	AAW44367	
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7.	7.5	163	7.7	AAG 3 0 4 0 5	Arabidopsis thalia
44 44	73.3	163	77	AAG50215	dopsis thal
4	13.3	7/7	77	AAG30404	thali
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				ALIGNMENTS	
KESULT I					
#7660I	7	1			
47550 IWW	standard;	peptide;		11 AA.	
AC AAY69924;					
XX 11 4000					
DT 11-APR-2000 XX	(Ilrst	t entry)	<u>~</u>		
Нишар	cyclophilin	B peptide		fragment #4.	
KW Cyclophilin KW HLA antigen;	B;	human; tu lagnosis;	tumour ans; tumour;	antigen peptide; ir; therapy.	cytotoxic T-cell; CTL;
OS Homo sapiens	è.				
AA WO9967288-A1	1				
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Gaps

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Mismatches

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Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or poly4+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs, and genomic
           This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5' ESTs are also used in diagnostic, forensic, gene therapy and
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                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
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                                                                                                                                                            100.0%; Score 60; DB 21; Length 11; 100.0%; Pred. No. 4.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.
                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duclert A,
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                                                                                                                                                                                                11; Conservative
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N-PSDB; AAC00096.
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Score 60; DB 21; Length 166; Pred. No. 0.00078;

100.0%; 100.0%;

Query Match Best Local Similarity

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The invention relates to a composition for modulating somatolactogenic function, comprising cyclophilin B (CypB), a mutant of cyclophilin B C function, comprising cyclophilin Which residues 2-12 of the mature protein are absent) or an inhibitor of the interaction of cyclophilin B with a comatolactogenic hormone (e.g., prolactin, growth hormone). The invention can also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for claspinsing diseases associated with abnormal somatolactogenic functions using CypB and a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic function in the animal, and cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic function, breasting cyclophilin B is useful in the treatment of immunosuppression, composition comprising cyclophilin B is useful in the treatment of immunosuppression, in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B with a somatolactogenic composition cyclophilin B with a somatolactogenic composition comprising cyclophilin B with a somatolactogenic composition cyclophilin B with a somatolactogenic composition comprising cyclophilin B with a somatolactogenic composition cyclophilin B with a somatolactogenic composition cyclophilin B with a somatolactogenic sequence represents a human cyclophilin B with a somatolactogenic concerve represents a human cyclophilin B with a somatolactogenic sequence represent sequence is not shown in the specification, but be a sequence is not shown in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone .
                                                                                                                                                                                                                                                                                                                                                                   Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteopprosis; HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia; c-terminal deletion mutant; mutein.
                                                                                                                                                                                                                                                                                                                         Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 211;
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Pred. No. 0.001;
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                                                                                                                                                                        AAB73302 standard; protein; 211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page -; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clevenger CV, Rycyzyn MA;
                                                                                                                                                                                                                                                                           22-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-211249/21.
1 GYKNSKFHRVI 11
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                            gyknskfhrvi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                            AAB73302;
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                                              87
                                                                                                                                                 AAB73302
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AAB43878 standard; Protein; 291 AA.

AAB43878

87

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08-FEB-2001 (first entry)

AAB43878;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for inhibiting somatolactogenic function in the animal. A composition comprising cyclophiln B is useful in the treatment of immunosuppression, in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising cyclophilin B mutant or a composition comprising hormone, is useful for treating HIV infection, breast and prostate cancer, gigantism/acromegaly, and hyperprolactinaemia. The present sequence represents human cyclophilin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone \,
                                                                                                                                                                                                                                                                                                                    Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia.
     Gaps
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     Indels
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 Mismatches
                                                                                                                                                                   AAB73301 standard; protein; 216 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0149752.
                                                                                                                                                                                                                                                                                  Human cyclophilin B (CypB).
                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clevenger CV, Rycyzyn MA;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-211249/21.
                                   1 GYKNSKFHRVI 11
                                                                     87 gyknskfhrvi 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200113113-A1
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                              22-MAY-2001
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include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antidiabetic; antiasthmatic; antirheumatic; antibacterial; antiviral; certific ammatological; neuroprotective; cardiant; thrombolytic; coagulant; coortropic; vasotropic; antipsoriatic and antiangiogenic. The noctropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Colynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating the proliferation, differentiation or mobilisation of cimmune cells, to treat disorders of haematopoietic cells, autoimmune cells, to treat disorders of haematopoietic cells, autoimmune cells; andulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and confirmant or ancers, cardiovascular disorders, neurological disease and confirmant or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to the massert invention.
                                                                                                                                                               diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiarthmatic; antirheumatic; antibarthritic; antiviral; antiniflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermacological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoiatic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer \dot{\cdot}
                                                                                                                                                cancer associated gene; cancer antigen; detection; cancer;
                                                                                               Human cancer associated protein sequence SEQ ID NO:1323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 1974-1975; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000; 2000WO-US05882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-587533/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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Gaps

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100.0%; Score 60; DB 22; Length 216; 100.0%; Pred. No. 0.001; Live 0; Mismatches 0; Indels (

Ouery Match 100. Best Local Similarity 100. Matches 11; Conservative

1 GYKNSKFHRVI 11

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Dictyostellum; DP1; discoldin II; human DP1; hDP1; cyclophilin; DdCyP2; bisphosphonate binding protein; calcium metabolism; cyclosporine; osteoporosis; hypercalcaemia; bone metabolism; bone metastases.
   D. discoideum cyclophilin (DdCyP2).
                                                                                                                                                                           (UYSH-) UNIV SHEFFIELD MED SCHOOL.
                                                                                                                                                                                                                                                                                               Claim 5; Fig 21; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.0%;
80.0%;
                                                                                                                         98WO-US02709
                                                                                                                                           97US-0039738
                                                                                                                                                                (PROC ) PROCTER & GAMBLE CO
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Conservative
                                                               Dictyostelium discoideum
                                                                                                                                                                                                                           WPI; 1998-506311/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
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64 ykdskfhrii 73
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                                                                                                                         13-FEB-1998;
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                                                                                  WO9836064-A1
                                                                                                      20-AUG-1998.
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                                                                                                                                                                                                                                                                                                                                                                    Novel cyclophilin, endogenous to e.g. Dirofilaria immitis, useful for identifying compounds and for treating parasitic infections which are not susceptible to cyclosporin A, comprises a tyrosine residue in drug-binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a cyclophilin including a tyrosine residue in the drug-binding site, and which is endogenous to the parasites Onchocerca volvulus, Brugia malayi, Dirofilaria immitis. The cyclophilin is useful for inhibiting the growth and development of parasites or for treating parasitic infections which are not susceptible to cyclosporin A. The purified 'tyrosine-containing' cyclophilin can be used to produce antibodies, either polyclonal or cyclophilins in other parasites.
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Pred. No. 0.15;
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              Indels
    Pred. No. 0.0014;
Mismatches 0;
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                                                                                                                                                                  Caenorhabditis elegans cyclophilin CeCyp-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                       AAB49141 standard; Protein; 171 AA
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                                                                                                                                                                                                                                                                                                           (NEWE ) NEW ENGLAND BIOLABS INC.
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90.0%;
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               11; Conservative
                                                                                                                                                                                      Cyclophilin; tyrosine;
                                                                                                                                                                                                         Caenorhabditis elegans
                                              WPI; 2001-079415/09
                                  1 GYKNSKFHRVI 11
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Matches 9; Conserv
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|SS ykgskfhrvi 64
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 AA;
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                Matches
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                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This represents the amino acid sequence of cyclophilin (DdCyP2) from the Dictyostellum discoldeum Ax-2. The invention provides sequences encoding Dictyostellum Path, human DP1, human DP1 (abP1) and Dattyostellum Cyclophilin (DdCyP2) which are bisphosphonate binding proteins. The invention also provides methods for burifying and producing such bisphosphonate binding protein, or an antibody which binds to the binding protein can be used in the diagnosis of calcium metabolism disorders. They can also be used to treat calcium metabolism disorders, where the treatment is for the regulation of bone metabolism.
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                                                                                                                                                                                                                                                       Bisphosphonate binding protein - used to treat calclum metabolism disorders, including bone metabolism, hypercalcaemia, bone metastases, and osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypercalcaemia, bone metastases, and osteoporosis, especially by regulation of bone metabolism via interaction with cyclosporine.
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    J1 X, Rogers MJ;
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Pred. No. 0.16;
2; Mismatches
Cook JS, Ebetino·FH, Ibbotson KJ,
Russell RGGR, Watts DJ, Xiong XJ;
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03-NOV-1999;
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05-MAR-1999;
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                                                                                                                                                                                                                                     AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; adenine nucleotide translocator; ANT; MTP; cyclophilin D; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                            Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB 2
Pred. No. 0.17;
0; Mismatches
                                                                                                                                                                                                                    Claim 11; Page 1699-1700; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU01197 standard; Protein; 207 AA.
                                                                                           (HUMA-) HUMAN GENOME SCI INC
(ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                80.0%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cyclophilln D protein.
                                                  08-MAR-2000; 2000WO-US05988
                                                                       99US-0124270
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Matches 9; Conservative
                                                                                                                         Rosen CA, Ruben SM;
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                                                                       12-MAR-1999;
                              21-SEP-2000.
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mitochondrial core components e.g. adenine nucleotide translocator (ANT) proteins are mitochondrial core components e.g. adenine nucleotide translocator (ANT) proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial component polypeptide (e.g. ANT) fused to an energy transfer promoter operably linked to a polynucleotide encoding a mitochondrial component polypeptide (e.g. ANT) fused to an energy transfer component polypeptide (e.g. ANT) fused to an energy transfer consecution (ETP) or a FLASH sequence). The novel expression construct can alter mitochondrial core components. The methods are useful for screening for a mitochondrial function or dysfunctional cell survival. These agents are useful for the prevention or treatment of diseases associated with altered consecution or dysfunctional cell survival, such as mitochondrial function or dysfunctional cell survival, such as a mitochondrial encephalopathy, lactic acidosis, and stroke, hyperproliferative disorders e.g. cancer, and deafness.
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                                                                                                                                                                                                                                                                                                                                                        New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynuclectide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule.
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                                                                                                                                            Wiley SE, Andreyev AY, Frigeri LG;
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Pred. No. 0.19;
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                                                                                                                                        Murphy AN, Clevenger W,
Velicelebi G, Davis RE;
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US-0123548 US-0125788 US-0126264 US-0126785 US-0127462 US-0127462 US-0127462 US-0127462 US-013047 US-013069 US-013069 US-013069 US-013069 US-013069 US-013069 US-013069 US-013069 US-013069 US-013069	9905-0132484. 9905-0132485. 9905-0132486. 9905-0132863. 9905-0132863. 9905-0134286. 9905-013421. 9905-0134370. 9905-0134370. 9905-0134370. 9905-0134370. 9905-0134370. 9905-0134370. 9905-0134370. 9905-0134370. 9905-0134370. 9905-0134370. 9905-0134370. 9905-0134370.	905 - 0139458 905 - 0139459 905 - 0139460 905 - 0139461 905 - 0139461 905 - 0139462 905 - 0139763 905 - 0139763 905 - 0140354 905 - 0140354 905 - 0141842 905 - 0141842 905 - 0142803 905 - 0142803
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706-MAY-1999;
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Pred. No. 0.23;
1; Mismatches 2; Indels
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990S-0157865.
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990x5-0144334.
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28-SEP-19
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
 Gaps
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0
 DB 21; Length 254;
 Indels
 Arabidopsis thaliana protein fragment SEQ ID NO: 17118.
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Pred. No. 0.24;
0; Mismatches
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 80.0%;
81.8%;
 25-FEB-2000; 2000EP-0301439
 17-OCT-2000 (first entry)
 Best Local Similarity 81.8
Matches 9; Conservative
 Arabidopsis thaliana
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AAG16462
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PR 25 - JUL. 1999 99105-0145224

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PR 72 - JUL. 1999 99105-0145217

PR 72 - JUL. 1999 99105-0145218

PR 73 - JUL. 1999 99105-0145218

PR 74 - JUL. 1999 99105-0145218

PR 75 - JUL. 1999 99105-0155218

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                                                                                                                           Gaps
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                                                                                                                Gaps
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1; Mismatches 2; Indels
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80.0%; Score 48; DB 19; Length 3224; 81.8%; Pred. No. 3.7; ive 1; Mismatches 1; Indels (

Query Match Best Local Similarity 81.8%;

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1 GYKNSKFHRVI 11
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Sequence 14,
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Sequence 13,
Sequence 12,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PerUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/peruS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-145-995A-13

US-08-145-995A-13

US-08-134-852-13

US-08-142-897-8

US-08-142-897-8

US-08-142-897-9

US-09-134-852-9

US-09-134-852-9

US-08-145-995A-11

US-08-145-995A-11

US-08-145-995A-11

US-08-145-995A-11

US-08-145-995A-11

US-08-145-995A-11

US-08-145-995A-11

US-08-141-747-11

US-08-142-995A-11
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                                                                                                                                                                                                                                                                                                    212252 segs, 22503292 residues
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                                                                                                    January 15, 2002, 13:03:59

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                      seq length: 0 seq length: 2000000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
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 Sequence 3, Appli
Sequence 18, Appl
Sequence 6, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 14, Appl
Sequence 16, Appl
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Sequence 10,
Sequence 3, P
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Sequence 3, P
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                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: 6 Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
US-08-989-386-3
US-08-944-604-20
US-08-944-604-18
US-08-482-728A-19
US-08-482-728A-19
US-08-09-028-366-4
US-08-142-897-9
US-08-142-897-9
US-08-145-958A-14
US-08-134-852-14
US-09-134-852-14
US-08-451-747-10
US-08-451-747-10
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                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.0
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: unkr
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ADDRESSEE: Flehr, Hobbach, Test, Albritton
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US-08-145-995A-13
                        ADDRESSEE:
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                                                                                                                                                                           APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: NO. 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 0.001;
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Sequence 11.

Patent No. 5968802

GENERAL INFORMATION:

APPLICANT: Wang, Bruce
APPLICANT: Fayner, Joseph
APPLICANT: Payne, Donald
APPLICANT: No. 5968802e1 Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy D.
RECISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECHOME: 415-326-2400
TELECHOME: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34,587
ER: 5490A-92-1
                                                                                                                  Sequence 7, Application US/08142897
Patent No. 5447852
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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; MOLECULE TYPE: protein
US-08-142-897-7
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    30 GYKNSKFHRVI 40
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Patent No. 5482850

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CALCW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: DAVID G. CONLIN: DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54; DB 2; Length 126
Pred. No. 0.0072;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 130 WAPER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                       COMPUTER: TELEPOPY disk
COMPUTER: TIBM PC COMPATIBLE
COMPUTER: TIBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REGISTRATION NUMBER: 38,304
REGISTRATION NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
E: & Herbert
Four Embarcadero Center, Sulte 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 amino acids
                                                                                        COUNTRY: United States ZIP: 94111-4187
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 90.0
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-482-728A-11
                                         CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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STRANDEDNESS: unl
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Gaps

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Fatent No. 6127148
GENERAL INPORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: USHMAN
STREET: 130 WATER STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 161;
                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
      Best Local Similarity 81.8%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53; DB 3;
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
ATTORNEY AGENT INFORMATION:
NAME: RESNICK, DAVID S:
REGISTATION NUMBER: 34.346
REFERRUCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.3%;
81.8%;
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Best Local Similarity 81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 161 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-134-852-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                   1 GYKNSKFHRVI 11
                                                                                                44 GYKGSKFHRII 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-08-482-728A-12
                                                                                                                                                                                              US-09-134-852-13
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STREET: 32 TOZER ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-451-747-13
Sequence 13, Application US/08451747
Patent No. 5821107
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    88.3%; Score 53; DB 1; Length 161; 81.8%; Pred. No. 0.014; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.3%; Score 53; DB 2; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATIN APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA;
APPLICATION UNBER: US 08/145,995
FILING DATE: 29-CT-1993
CLASSIFICATION: 514
ATORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMUNICATION INFORMATION:
TELECHIONE: (508) 927-5054
TELEFRAX: (508) 927-1705
REFERENCE/DOCKET NUMBER: 43406
             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEPHONE: (617) 523-3400
TELEPHONE: (617) 523-34640
TELEPHONE: (617) 523-3640
TELEPHONE: (617) 523-3640
TELEPHONE: (617) 523-3640
TELEPHONE: (617) 523-3640
TELEPHONE: 101 0 00: 13: 580UENCE: LENGTH: 11 0 00: 13: 580UENCE: TYPE: amino acid TYPE: amino acid STRANDEDNESS: unknown TOPOLOGY: unknown 1: MOLECULE TYPE: protein US-08-145-995A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
                                                                                                                                                                                                                                                                                                                  Query Match 88.3
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-451-747-13
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                                                                                                                                                                                                                                                                                                                                                                                                     1 GYKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: unb
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Gaps

Query Match

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APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 163;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FLING DATE: 29-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                              PRIOR APPLICATION DATE:
APPLICATION UNMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTONNEY, ACGINI INFORMATION:
NAME: Dunn, Tracy D.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEFHONE: 415-326-2400
TELEFAX: 415-326-2402
INFORMATION FOR SEG ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48;
Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 434(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEFX: 200291 STRE UR
INFORMATION FOR SED ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.0%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 163 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 80.0
Best Local Similarity 72.7
Matches 8; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-142-897-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
APPLICATION NUMBER:
FILING DATE: 15-JA
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46 GYKGSSFHRII 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-08-145-995A-9
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Sequence 8, Application US/08142897

Sequence 8, Application US/08142897

Patent No. 5447895

APPLICANT: Friedman, Jeffrey S.

APPLICANT: Weissman, Irving L.

TITLE OF INVENTION: and Uses

TITLE OF I
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No. 5968802el Nuclear Cyclophilin
21
                                                                                                                                                                                    STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
21P: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGRNT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 38,304
REGISTRATION POR SEO ID NO: 12: SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
                               NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.08
0; Mismatches
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: protein
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GYKNSKFHRVI 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-482-728A-12
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GENERAL INFORMATION:
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US-09-028-366-7
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                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
                                                       DB 1; Length 164; 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 164;
                                                                                        2; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
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Pred. No. 0.12;
                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
RECISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMONIACATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
                                                       Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-CCT-1993
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REGARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                          RESULT 10
US-08-451-747-9
Sequence 9, Application US/08451747
; Patent No. 5821107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 9, Application US/09134852
; Patent No. 6127148
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72.7%;
                                                     80.0%;
72.7%;
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                                                   Query Match 80.0
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-451-747-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: unk
                                                                                                                     1 GYKNSKFHRVI 11
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47 GYKGSSFHRII 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 01915
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US-08-145-995A-9
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US-09-134-852-9
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APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                             ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
CITY: BOSTON
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09028366

Patent No. 6150501

GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: HONG, XIOIANG
APPLICANT: MA, DONG
TITLE OF INVENTION: NOVEL TYROSINE-CONTAINING
TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/134,852 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-OCT-1993
ATTORNEY AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: New England Biolabs, Inc.
STREET: 32 Tozer Road
CITY: Beverly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 43406 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-134-852-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS: un)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYKNSKFHRVI 11
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Gaps
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                                                                                                                                   Length 3224;
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                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                     Sequence 34, Application US/08989045
Patent No. 6027905
GENERAL INFORMATION:
APPLICANT: RESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DETECTION OF CERVICAL CANCER
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,045
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INPORMATION:
NAME: GREENHALGH, DUNCAN A
REGISTRATION NUMBER: 38,678
REGISTRATION NUMBER: 38,678
REFERENCE/DOCKET NUMBER: 4MP-023 (8395/27)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3224 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 3;
Pred. No. 2.6;
1; Mismatches
                                                                                                                                    DB 2;
                                                                                                                                 Score 48; DB 2;
Pred. No. 2.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-482-728A-15
; Sequence 15, Application US/08482728A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
                                                                                                                                   80.0%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%;
81.8%;
LENGTH: 3224 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                   Query Match
Best Local Similarity 81.0.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 80.0
Best Local Similarity 81.8
Matches 9; Conservative
                                               TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-705-660-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3107 GFKNSIFHRVI 3117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                      1 GYKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                           RESULT 14
US-08-989-045-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/08705660
Patent No. 5858683
GENERAL INFORMATION
GENERAL INFORMATION:
THORMATION:
TILLE OF INVENTION:
MUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: WA
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 4
Pred. No. 0.12;
0; Mismatches
       SOFTWARE: FASTEM: DOS
SOFTWARE: FASTESO VETSON 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,366
FILING DATE:
                                                                                                                                                                                                                         NEB-133
                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-
TELECOMUNICATION INFORMATION:
TELEPHONE: 978-927-5054
TELEFAX: 978-927-1705
                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%;
90.0%;
   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 80.0
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-028-366-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 YKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 YKGSKFHRVI 64
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GENERAL INFORMATION:

APPLICANT: Wang, Bruce
APPLICANT: Payan, Donald
TTILE OF INVENTION: No. 5968802el Nuclear Cyclophilin
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flebr, Hobbach, Test, Albritton
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
CITY: San Francisco
STATE: California
COUNTRY: United States
21P: 94111-4187
COMPUTRR READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRY: IDM PC Compatible
OPERATING SYSTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: READABLE: 07-JUN-1995
CLASSIFICATION NUMBER: 38,304
FILING DATE: 07-JUN-1995
STELERA: (415) 398-1349
TELECOMMUNICATION INFORMATION:
NAME: S1194 ROBIN M.
RESTERENCE, COMPUTE: (415) 398-1349
TELECOMMUNICATION INFORMATION:
TE
```

0; Gaps 2; Indels Query Match 76.7%; Score 46; DB: Best Local Similarity 81.8%; Pred. No. 0.2; Matches 9; Conservative 0; Mismatches 1 GYKNSKFHRVI 11 30 GYKGSIFHRVI 40 ò g

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DB 2; Length 126;

Search completed: January 15, 2002, 13:03:59 Job time: 215 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein

January 15, 2002, 13:06:15 Run on:

; Search time 42.04 Seconds (without alignments) 19.931 Million cell updates/sec

US-09-720-469-4 60 Perfect score:

1 GYKNSKFHRVI 11 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pirl:* 3: pir3:* 4: pir4:* PIR 68:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		df			SOMMALES	
Result		Query				
No.	Score	Match	Length DB	80	di .	Description
1	9	100.0	183	7	S71547	peptidylprolyl iso
7	9		208	٦	CSHUB	
m	60		216	C)	A56861	_
4	54	90.0	212	ď	A54204	
ഗ	23		161	~	A45000	_
Q	53		173	~	T39632	_
7	51	85.0	164	~	863995	prolyl
œ	20	83.3	207	N	A40516	_
σ	49	81.7	183	~	T18578	-
10	48		137	~	S68767	_
11	48		164	-	CSHYAC	_
12	48		164	Н	CSMSA	-
13	48	80.0	164	-	CSRTA	_
14	48		179	C)	JT0686	_
15	48		204	~	T21587	_
16	48		207	7	A41581	
17	48	80.0	223	П	CSNCM	
18	48		260	~	B53422	
91	48		3224	-	558884	o
20	47	78.3	201	N	T50837	peptidylprolyl iso
77	47		201	N	T02489	peptidylprolyl iso
7.7	47	78.3	201	~	T18573	peptidylprolyl iso
23	46		162	-	CSCK	peptidylprolyl iso
24	46	76.7	165	7	B38388	
25	46		212	7	A40047	peptidylprolyl iso
26	45		163	7	CSBOAB	_
27	45		163	,	CSPGA	peptidylprolyl iso
28	45	75.0	165	-	CSHUA	peptidylprolyl iso
56	45	75.0	199	~	F84808	Ę

		probable 40 kd pep	peptidylprolyl iso	peptidylprolyl iso	peptidylprolyl iso	_	_			-	lprolyl i	peptidylprolyl iso	· -	orc	hypothetical profe	14
	200024	S6232/	T10056	T06073	S51497	S71849	S66681	S28020	T27371	T27882	S71219	T27373	T27034	T23003	T21487	CSBY
c	9 (7	~1	7	~	7	٦	7	7	7	7	7	7	7	7	7
ני	4 1	356	172	172	180	227	301	165	171	172	173	173	192	523	795	162
7	0.0	0.6/	73.3	73.3	73.3	73.3	73.3	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	70.0
4	1 4	40	44	44	44	44	44	43	43	43	43	43	43	43	43	42
02	9.5	1	32	33	34	35	36	37	38	39	40	41	42	43	44	4 5

ALIGNMENTS

```
A. Experimental source: liver

C. Superfamily: peptidylprolyl isomerase; cyclophilin homology

C. Keywords: cis-trans-isomerase

F.1-183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental <MAT>

F;10-172/Domain: cyclophilin homology <CYP>
peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K · rat
N;Alternate names: cyclophilin B; PPIASE
C;Species: Rattus norvegicus (Norway rat)
C;Date: i5-Nov_1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
                                                                                                                                                C. Accession: S71547
R. Ruecknagel, K.P.; Pfelfer, T.; Rahfeld, J.U.; Schaerfke, M.; Fischer, G. submitted to the Protein Sequence Database, November 1996
A. Reference number: S71547
A. Rocession: S71547
A. Molecule type: protein
A. Residues: 1-183 < RUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 60; DB 2; Length 183; 100.0%; Pred. No. 0.00044;
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; 0 Indels 0; Mismatches Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative

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1 GYKNSKFHRVI 11 111111111 54 GYKNSKFHRVI 64 g δ

peptidylprolyl isomerase (EC 5.2.1.8) B precursor [validated] - human N;Alternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Dec-2000 C;Accession: A39118; A39722; A40515; S65742 R;Price, E.R.; Zydowsky, L.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T. R?Price, E.R.; Zydowsky, L.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T. A37118 A:Title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl iso A;Accession: A39118

A; Molecule type: mRNA A; Residues: 1-208 <PRI> A; Cross-references: GB:M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335 A; Cross-references: GB:M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335 B; Hasel, K.W.: Glass, J.R.; Godbout, M.; Sutcliffe, J.G. A; Hall: Biol: 11, 3484-3491, 1991 A; Title: An endoplasmic reticulum-specific cyclophilin. A; Reference number: A39722; MUID:g1260697

A;Molecule type: mRNA A;Residues: 1-208 <HAS> A;Cross-references: GB:M60457; NID:9181249; PIDN:AAA35733.1; PID:9181250

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90.08;
90.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-212 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                           A; Molecule type: mRNA
A; Residues: 9-216 <NOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HI HIHIII
81 GYKGSKFHRVI
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A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A45000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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A45000
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R; Spik, G.; Haendler, B.; Delmas, O.; Mariller, C.; Chamoux, M.; Maes, P.; Tartar, A.; M. J. Biol. Chem. 266, 10735-10738, 1991
A; Title: A novel secreted cyclophilin-like protein (SCYLP).
A; Reference number: A40515; WUID:91250363
A; Accession: A40515; WUID:91250363
A; Mccession: A40515
A; Mariller, C.; Allain, F.; Koucch, M.; Spik, G.
B; Mariller, C.; Allain, F.; Koucch, M.; Spik, G.
B; Mccession: S6574
A; Mccession: S6574
A; Mccession: S6574
A; Mccession: S6574
A; MulD:96186273
A; Mccession: S6574
A; MulD: Mull A; MulD:96186273
A; Mccession: S6574
A; MulD: Mull A; MulD:96186273
A; Mccession: S6574
A; MulD: Mull A; MulD:96186273
A; Mccession: S6574
A; MulD: Mull A; MulD:96186273
A; Mccession: S6574
A; MulD: Mull A; MulD:96186273
A; Mccession: S6574
A; MulD: Mull A; MulD:96186273
A; Mccession: S6574
A; MulD: Mull A; MulD:96186273
A; Mccession: S6574
A; MulD: Mull A; MulD:96186273
A; Mccession: S6574
A; MulD: Mull A; MulD:96186273
A; Mccession: S6574
A; MulD: Mull A; MulD:96186273
A; Mccession: S6574
A; MulD:96186273
A; Mccession: S6574
A; MulD:96186273
A; Mccession: S6574
A; MulD:96186273
A; Mccession: S6574
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A; Mccession: S6574
A; MulD:96186273
A; Mccession: S6574
A; MulD:96186273
A; Mccession: S6574
A; MulD:96186273
A; Mccession: S6574
A; MulD:96186273
A; Mul
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N:Alternate names: cyclophilin B; cyclophilin-S1; cyclosporin A-binding protein
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Accession: A56861; B39722; S21835
C;Accession: A56861; B39722; S21835
Biochim. Biophys: Acta 1129, 13-22, 1991
A;Title: Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a putative sign A;Reference number: A56861; MUID:92096454
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A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Mesidue: Lye: mRNA
A; Residues: L-216 < SCH>
A; Experimental source: teratocarcinoma F9 cells
A; Note: sequence extracted from NCBI Deschoone (NCBIN:73234, NCBIP:73239)
A; Note: parts of this sequence, including the amino end of the mature protein, were conf
R; Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
MOI. Cell Blol. 11, 3484-3491, 1991
A; Title: An endoplasmic reticulum-specific cyclophilin.
A; Reference number: A39722; MUID:91260697
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R;Nordheim, A.
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A:Reference number: S21835
A:Accession: S21835
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Best Local Similarity 100.
Matches 11; Conservative
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A; Molecule type: mRNA
A; Residues: 9-216 <HAS>
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Nicontains: cyclophilin
C;Species: Echinococcus granulosus
C;Date: 14-May-1993 *sequence_revision 14-May-1993 *text_change 08-Sep-2000
C;Accession: A45000
R;Lightowlers, M.W.; Haralambous, A.; Rickard, M.D.
Mol. Blochen, Parasitol. 36, 287-289, 1989
Mol. Blochen, Parasitol. 36, 287-289, 1989
A;Title: Amino acid sequence homology between cyclophilin and a cDNA-cloned antigen o
A;Reference number: A45000; MUID:90014983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: A44204
R; Schneider, H.; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurini, M.G.; Quesn Biochemistry 33, 8218-8224, 1994
A; Title: Human cyclophilin C; primary structure, tissue distribution, and determinati. A; Reference number: A54204; MUID:94304830
A; Cross-references: EMBL:X58990; NID:953034; PIDN:CAA41736.1; PID:953035
C; Comment: This protein is distinguished from peptidylprolyl isomerase A by the prese
C; Comment: This protein is distinguished from peptidylprolyl isomerase; cyclophilin homology
C; Keywords: Cis-trans: isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell
F;1-33/Domain: signal sequence #status predicted <SIG>F;34-216/Product: peptidylprolyl isomerase B #status predicted <MAT>F;43-205/Domain: cyclophilin homology <CYP>
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C;Date: 22-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
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A;Cross-references: GB:J04664; NID:g158843; PIDN:AAA29058.1; PID:g158844
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A;Experimental source: kidney
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C;Superfamily: peptidylprolyl isomerase; cyclophillin homology
C;Reywords: cis-trans-isomerase; cyclosporin A binding
F:37-199/Pomain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human N.Alternate names: cyclophilin C
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Pred. No.
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peptidylprolyl isomerase (EC 5.2.1.8) cyp-11 [similarity] - Caenorhabditis elegans
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C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C.Accession: T18578; T24269
R.Page, A.P.; MacNiven, K.
submitted to the EMBL Data Library, August 1995
A.Reference number: Z18986
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A:Molecule type: mRNA
Cross-references: 08:M63553; NID:g212648; PIDN:AAA49064.1; PID:g212649
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding
F;34-196/Domain: cyclophilin homology <CYP>
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C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase
F:16-183/Domain: cyclophilin homology <CYP>
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0.041;
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A;Molecule type: mRNA
A;Residues: 1-183 <-PAG>
A;Cross-references: EMBL:U34955; PIDN:AAC47115.1
A;Experimental source: strain Bristol N2
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Pred. No. 0.056;
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81.8%;
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Best Local Similarity
'-haq 9; Conserve
                                            GYKGSRFHKVI 57
               GYKNSKFHRVI 11
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78 GFKGSKFHRVI 88
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Best Local Similarity
Matches 9; Conserv
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N.Alternate names: cyclophilin
C.Species: Blattella germanica (German cockroach)
C.Species: Blattella germanica (German cockroach)
C.Bate: 2-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C.Accession: S63995
R.Martinea-Gonzalez, J.; Hegardt, F.G.
Eur. J. Blochem. 234, 284-292, 1995
A.Title: Characterization of a cDNA encoding a cytosolic peptidylprolyl cis-trans-isomer
A.Reference number: S63995, MUID:96096751
A.Status: preliminary
A.Molecule type: mRNA
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-164 cAMA.
A.Cross-references: EMBL:X87418; NID:91235942; PIDN:CAA60869.1; PID:91772496
C.Superfamily: peptidylprolyl isomerase; cyclophilin homology
C.Keywords: cis-trans-isomerase
F;3-164/Domain: cyclophilin homology <CYP>
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Niconatains: cyclopillin
Niconatains: cyclopillin
Niconatains: cyclopillin
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 08-Sep-2000
C;Accession: T3963 #sequence_revision 03-Dec-1999 #text_change 08-Sep-2000
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
A;Rocession: T39632
A;Accession: T39632
A;Accession: T39632
A;Accession: T39632
A;Accession: T39632
A;Rocession: T39632
A;Rocession: T39632
A;Rocession: T39632
A;Rocession: T39632
A;Rocession: T37 < CINN
A;Coss-references: EMBL;AL031852; PIDN:CAA21243.1; GSPDB:GN00067; SPDB:SPBC1709.04c
A;Rocession: T37 < CINN
A;Coss-references: EMBL;AL031852; PIDN:CAA21243.1; GSPDB:GN00067; SPDB:SPBC1709.04c
C;Gonetics:
A;Roperimental source: strain 972h-; cosmid c1709
C;Gonetics:
A;Roperimental source: strain 972h-; fo/3
A;Introns: 10/3: 32/2; 38/2; 54/1; 76/3
C;Superfamily: peptidylprolyl isomerase; cyclophillin homology
C;Keywords: cis-trans-isomerase
F;4-173/Domain: cyclophillin homology CCYP>
                                                                                                                                                                                                                                                                                                                                                                                                         peptidylprolyl isomerase (EC 5.2.1.8) u-snrnp-associated SPBC1709.04c [similarity] - fis
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                                                                                                                                 Score 53; DB 2; Length 161;
Pred. No. 0.0084;
1; Mismatches 1; Indels
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81.8%; Pred. No. 0.009;
ive 1; Mismatches 1; Indels
  peptidylprolyl isomerase; cyclophilin homology
C;Superfamily: peptidylprolyl isomerase; c;
C;Keywords: cis-trans-isomerase
F;1-161/Domain: cyclophilin homology <CYP>
                                                                                                                                 88.3%;
81.8%;
                                                                                                                              Query Match 88.3
Best Local Similarity 81.6
Matches 9; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
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54 GYKNSTFHRII 64
                                                                                                                                                                                                                                                                                                                                                                                                                                      N: Contains: cyclophilin
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Matches 9; Conserv
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A;MOlecule type: mRNA
A;Residues: 100-148, MARPARRSPSPTVGNSNFFDLRAFYPSNH','SFCSSGEHPHPICSQYPVISALTEVLWVP','
A;Cross-references: EMBL:M25637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds C; Superfamily: peptidylprolyl isomerase; cyclophilin homology C; Keywords: cis-trans-isomerase; cyclosporin A binding; DNA binding; macrophage; T-ce F;3-164/Domain: cyclophilin homology CCPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptidylproly1 isomerase (EC 5.2.1.8) A - rat
N.Alternate names: 13.3K protein [misidentification]; cyclophilin A; cyclosporin A-bi
C;Species: Rattus norvegicus (Norway rat)
C;Dace: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 04-Feb-2000
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 04-Feb-2000
C;Accession: A29819; A60036; A15632; A58829
R;Danielson, P.E.; Forss-Petter, S.; Brow, M.A.; Calavetta, L.; Douglass, J.; Milner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A60036
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                 A;Cross-references: GB:X52803; NID:950620; PIDN:CAA36989.1; PID:950621
R;Krummrel, U.; Bang, R.; Schmidtchen, R.; Brune, K.; Bang, H.
FEBS Lett. 371, 47-51, 1995
A;Title: Cyclophilin-A is a zinc-dependent DNA binding protein in macrophages. A;Reference number: S66416; MUID:95394146
A;Accession: S66416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-164 cDN3
A; Cross-references: GB:M19533; NID:g203701; PIDN:AAA41009.1; PID:g203702
A; Cross-references: GB:M19533; NID:g203701; PIDN:AAA41009.1; PID:g203702
R; Lad, R.P.; Smith, M.A.; Hilt, D.C.
Brain Res. Mol. Brain Res. 9, 239-244, 1991
Brain Res. Mol. Brain Res. 9, 239-244, 1991
A; Title: Molecular cloning and regional distribution of rat brain cyclophilln.
A; Reference number: A60036; MUID:91232390
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A; Residues: 1-164 <LAD>
A; Experimental source: brain
B; Theodor, L.; Peleg, D.; Meyuhas, O.
Biochim. Biophys. Acta 826, 137-146, 1985
A; Title: P31, a mammalian housekeeping protein encoded by a multigene family
A; Reference number: A15632; MUID:86026347
A; Accession: A15632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: p1815: A cDNA clone of the rat mRNA encoding cyclophilin. A,Reference number: A29819; MUID:88283345
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A; Residues: 2-21 <KRU>
A; Experimental source: nuclear cyclophilin of H4-7 cells
C; Genetics:
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Pred. No. 0.077;
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A; Reference number: S10327; MUID:90326555
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A;Molecule type: mRNA
A;Residues: 1-164 <MEY>
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ilarity 72.78;
Conservative
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Best Local Similarity
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                                                                                             A; Residues: 1-164 <HAS>
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submitted to GenBank,
                                                                  A; Molecule type: mRNA
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A; Accession: A58859
                                    A; Accession: S10327
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CypA
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Nilernate names: cyclophilin A: cyclosporin A-binding protein A
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 31-Mar.1992 #sequence_revision 31-Mar.1992 #text_change 16-Jul-1999
C;Accession: S07597
R;Bergama, D.J.; Sylvaster, D.
Nucleic Acids Res. 18, 200, 1990
A;Title: A Chinese hamster ovary cyclophilin cDNA sequence.
A;Reference number: S07597; MUID:90174932
A;Accession: S07597
A;Molecule type: mRNA
A;Residues: 1-164 <ABER>
A;Cross-references: EMBL:X17105; NID:949495; PIDN:CAA34961.1; PID:949496
C;Function:
A;Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase; cyclopprin A binding: T-cell
F;3-164/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                   peptidylprolyl isomerase (EC 5.2.1.8) - rat (fragments)

NiAlternate names: cyclophilin

NiAlternate names: cyclophilin

C;species: Rattus norvegicus (Norway rat)

C;species: A: Varial, s.; Andreeva, L.; Totty, N.F.; Hsuan, J.J.; Ward, J.M.; Crompton,

Eur. J. Blochem. 238, 166-172, 1996

A;Reference number: S68767; MUID:96248435

A;Reference number: S68767; MUID:96248435

A;Reference number: S08767; MUID:96248435

A;Reference number: Norve: Inver

A;Residues: 1-13:14-22;23-29;30-60;61-77;78-100;101-114;115-137 <TAN>

A;Residues: 1-19:14-22;23-29;30-60;61-77;78-100;101-114;115-137 <TAN>

C;Superfamily: peptidylprolyl isomerase; cyclophilin homology

C;Reywords: cis-trans-isomerase; cyclosporin A binding; mitochondrion
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N;Alternate names: cyclophilin A: cyclosporin A-binding protein A
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Bate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: S10327; S66416; S40742
R;Hasel, K.W.; Sutcliffe, J.G.
Nucleic Acids Res. 18, 4019, 1990
A;Title: Nucleotide sequence of a cDNA coding for mouse cyclophilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 0.077;
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81.8%; Pred. No. 0.064;
iive 0; Mismatches
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         GYKNCTFHRVI 75
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Best Local Similarity
Matches 9; Conserv
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A; Gene: CESP: F31C3.1
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NiAlternate names: cytolophilin A
C:Species: Pusarium sporotrichioides
S:Chow. Lp.: Juden 1995
A:Restence number: J70686
A:Nolecule type: Protein
A:Restence number: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Restruction: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Restruction: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Restruction: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Restruction: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Restruction: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Restruction: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Restruction: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Restruction: Amno acid sequence of peptidyl-prolyl isomerase a of Fusarium sporotrich
A:Restruction: Amno acid sequence of peptidyl-prolyl isomerase: cyclophilin homology
C:Reyords: 1179 ccH2
A:Restruction: Amno acid sequence of peptidyl-prolyl isomerase: cyclophilin homology
C:Reyords: cis-trans: Isomerase: cyclosporin A binding: cytosol; nucleotide-binding mete: phosphate (Th:) (Covalent) (by protein kinase II) *status predicted
F:137/Binding site: phosphate (Th:) (covalent) (by protein kinase II) *status predicted
F:132/Binding site: phosphate (Th:) (covalent) (by casein kinase II) *status predicted
F:132/Binding site: phosphate (Th:) (covalent) (by covalent) (by covalent) (by covalent) (by Covalent)
F:132/Bindin
Note: the submission to GenBank in entry RATP31 is acknowledged as an unpublished erra
Comment: This protein belongs to a class of highly conserved proteins, abundant in thy
                                                                C;Function:
A;Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase; cyclosporin A binding; T-cell
F;3-164/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptidylproly1 isomerase (EC 5.2.1.8) F31C3.1 [similarity] - Caenorhabditis elegans
N;Contains: cyclophllin
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1; Mismatches
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Best Local Similarity 72.7
Matches 8; Conservative
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47 GYKGSSFHRII 57
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58 GYKGSSFHRII 68
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Matches 8; Conserv
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                      #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                          A;Introns: 69/3
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Reywords: cis-trans-isomerase
F;28-190/Domain: cyclophilin homology <CYP>
                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
0.097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 *sequence_revision 15-Oct-
R;Cottage, A. R:Cottage, A. Submitted to the EMBL Data Library, March 1997
A;Reference number: 219446
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48;
Pred. No.
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                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-204 <WIL>
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January 15, 2002, 13:14:59 ; Search time 24.88 Seconds (without alignments) 16.210 Million cell updates/sec Run on:

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Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		DI	CYPB_HUMAN	CYPB_MOUSE	CYPB_BOVIN	CYPC_HUMAN	CYPH_ECHGR	CYPB_RAT	CYPH_BLAGE	CYPB_CHICK	CYPB_CAEEL	CYPH_CRILO	CYPH_MOUSE	CYPH_RAT	CYP5_CAEEL	CYPM_RAT	CYPM_HUMAN	CYPH_NEUCR	CYP4_ARATH	RBP2_HUMAN	CYP6_CAEEL	CYPH_CANAL	CYPH_DROME	CYPC_MOUSE	CYPH_BOVIN	CYPH_HUMAN	CYPD_YEAST	CYP1_ARATH	CYPH_CATRO	CYPE_MOUSE	CYPE_DROME	CYPE_HUMAN	CYPH_ALLCE	CYPH_UROFA	PP1_STRCH
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RESULT

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E	(NEI, 40, LASE AMMODALION UPDATE) OLVI, CIG-TRANG ISOMEDASE D DEBCTESOD (EC. 2, 2, 0,
DE	(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLE) (CYCLOPHILIN B)
GN	PPIB OR CYPB.
SO	
ဗ ဗ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
3 8	Primates;
S S	NCb1_1dX1D=9000;
20	SECTION BY A AND CHORNOS OF SELAC
RX	56714; PubMed*2000394:
RA	Price E.R., Zydowsky L.D., Jin M., Hunter C.H., McKeon F.D.,
RA	
RŢ	"Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-
E E	
N N	FIOC. Mart. Acad. 5C1. U.S.A. 88:1903-1907(1991).
R D	A MORE SOURCE
RX.	MEDI.INE_G126363. Buhmed=2040602.
RA	Spik G., Heendler B., Delmas O., Mariller C. Chamony M. Maes D
RA	rades o
RA	Hiestand P.C., Movva N.R.:
RT	"A novel secreted cyclophilin-like protein (SCVID) ".
RL	J. Biol. Chem. 266:10735-10738(1991).
RN	[3]
КР	SEQUENCE OF 2-208 FROM N.A.
RX	MEDLINE=91260697; Pubmed=1710767;
RA	Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;
RT	
RL	Mol. Cell. Biol. 11:3484-3491(1991).
RN	[4]
RP P	SEQUENCE OF 64-76 AND 151-157.
X i	MEDLINE=93162043; Pubmed=1286667;
Ϋ́	Kasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
KA KA	
Z E	"Microsequences of 145 proteins recorded in the two-dimensional gel
¥ ;	protein database of normal human epidermal keratinocytes.";
7 2	Electrophoresis 13:960-969(1992).
Z C	[5]
r X	SOBCELLOLAR LUCATION, MEDITURE 92112948 - Dubmod 1520044.
RA	Arber S. Krause K H. Caroni B.
RŢ	"S-cvclobhilin is retained intracallularly via a unique codu-townia."
RT	sequence and colocalizes with the calcium storage protein
RT	Ireticulin.";
Z:	J. Cell Biol. 116:113-125(1992).
Z i	
ž 2	A*-KAR CRYSTALLOGRAPHY (1.85 ANGSTROMS).
A A	MEDLINE=942>3-45); FUDMOG=819/205; Mikol V Kallon T Gelbinoh M
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MEDLINE-94283623; PubMed-8013656; Galat A., Bouet F.;
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P80311;
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CYPB_BOVIN
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01-MAR-1992 (Rel. 21, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-SI).
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"x-ray structure of a cyclophilin B/cyclosporin complex: comparison with cyclophilin A and delineation of its calcineurin-binding
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                       Proc. Natl. Acad. Sci. U.S.A. 91:5183-5186(1994).

-i. FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

-i. CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

-i. ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.

-i. SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.

-i. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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208 PREVENT SECRETION FROM ER.
22742 MW; A814481B7EBD4579 CRC64;
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Multigene family; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 AA.
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EMBL; M63573; AAA36601.1; ALT_INIT.
EMBL; M60457; AAA35733.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR002130; CSA_PPIase.
Pfam: PF00160; pro_isomerase: 1.
PRNINTS; PR00153; CSAPPIARASE.
PROSITE: PS00170; CSA_PPIASE_1: 1.
PROSITE: PS50072; CSA_PPIASE_2: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB; 1CYN; 29-JAN-96,
Aarhus/Ghent-2DPAGE; 117; NEPHGE.
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Best Local Similarity 100.
Matches 11; Conservative
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199 2
208 AA;
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PIR; A40515; A40515.
PDB; 1CYN; 29-JAN-96
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                                                                          domain.
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CYPB_MOUSE
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
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PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
PREVENT SECRETION FROM ER
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
Schumacher A., Schroeter H., Multhaup G., Nordheim A.;
"Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a
putative signal sequence expressed in differentiating F9 cells.";
Blochim. Blophys. Acta 1129:13-22(1991).
-!- FUNCTION: PPRASES ACCELERATE THE FOLDING OF PROTEINS.
-!- FUNCTION: PPRASES ACCELERATE THE POLDING OF PROLINE IMIDIC
-!- FUNCTION: PROMES IN OLIGOPEPTIDES.
-!- BRAYME REGULATION: CYCLOSPORIN A (CSA) INHEBITS CYPB.
-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARI
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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Prints; PR00160; pro_isomerase; 1.
PRINTS; PR00155; CSA_PPISKRASE.
PROSTTE; PS00170; CSA_PPIASE_1; 1.
PROSTTE; PS50072; CSA_PPIASE_2; 1.
Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
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Carrello A., Mark P.J., House A.K., Ratajczak T.;
Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
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4B8DF5AE40BAD3A7 CRC64;
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MGD; MGI:97750; Ppib.
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PIR; S21835; S21835.
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Best Local Similarity
Matches 11; Conserv
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CYPH_ECHGR
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CYPH_ECHGR
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAWASE)
(CYCLOPHILIN C).
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"Cyclophilin-B is an abundant protein whose conformation is similar
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                                                                                                                                                                                                                                                                                                                                                                     --- FUNCTION: PPTASES ACCELERATE THE FOLDING OF PROTEINS.
--- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
---- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
---- SUBCELLULAR LOCATION: ENDOPLASMIC RETICCLUM LUMB.
---- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                    MEDLINE-94280416; PubMed-8010972;
Bose S., Muecke M., Freedman R.B.;
The characterization of a cyclophilin-type peptidyl prolyl
cls.trans-isomerase from the endoplasmic-reticulum lumen.";
Biochem. J. 300:871-875(1994).
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0097C88289AF6276 CRC64;
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Pfam: PF00160; pro_isomerase; 1.
PRNINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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208 AA; 22701 MW;
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                                           to cyclophilin-A.";
FEBS Lett. 347:31-36(1994).
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P45877:
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01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-90014983: PubMed-2677720;
Lightowlers M.W., Haralambous A., Rickard M.D.;
"Amino acid sequence homology between cyclophilin and a cDNA-cloned antigen of Echinococcus granulosus.";
mol. Biochem. Parasitol. 36:287-290(1989).
-!- FUNCTION: PPIASES ACCELEBRATE THE POLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- EXYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
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                    PEPTIDE BONDS IN OLIGOPEPTIDES.
--- BUXYME RECULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.
--- SUBCELLULAR LOCATION: CYTOPLASMIC.
--- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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Neodermata; Cestoda; Eucestoda; Cyclophyllidea; Taeniidae;
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Pred. No. 0.0041;
Tred. Treatments 1; Indels
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SEQUENCE 212 AA; 22763 MW; 6F3DB547A2AE581B CRC64;
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Pfam; PF00160; pro_isomerase; 1.
PRNUTS; PR00153; CSAPPIBARASE.
PROSITE; PS00170; CSA_PPIBASE_1; 1.
PROSITE; PS50072; CSA_PPIBASE_2; 1.
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Best Local Similarity 90.9
Matches 10; Conservative
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Arber S., Krause K.-H., Caroni P.;
"S-cyclophilin is retained intracellularly via a unique COOH-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 22, Last annotation update)
19-NOV-1995 (Rel. 21, Last annotation update)
19-PEPTIDYL-PROBYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                                             Score 53; DB 1; Length 161; Pred. No. 0.0047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence and colocalizes with the calcium storage protein calreticulin.";
                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDYL-PROLYL CIS-TRANS PREVENT SECRETION FROM ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
76D12AC3427FEF32 CRC64;
                                                                                                                                                                                   161 AA; 17223 MW; 72661E2F4FEF466F CRC64
                                                                                                                                         Cyclosporin; Isomerase; Rotamase; Multigene family.

NON TER

SEQUENCE 161 AA; 17223 MW; 72661E2F4FEF466F CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P23284; ICYN.
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                     PIR; A45000; A45000.

HSSP, P05092; 3CYS.

InterPro; IPR002130; CSA_PPIase.

Pfan; PF00160; pro_isomerase; 1.

PROSITE; PS00170; CSA_PPIASE_1; 1.

PROSITE; P550072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90300692; PubMed-2194066; Iwai N., Inagami T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kidney Int. 37:1460-1465(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23025 MW;
                                                                                                                                                                                                                                               88.3%;
81.8%;
    J04664; AAA29058.1;
                                                                                                                                                                                                                                                 Query Match 88.3
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS TO C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
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208
208
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                                                                                                                                                                                                                                                                                                                             1 GYKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
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Score 52; DB 1; Length 208; Pred. No. 0.0095;

86.7%; 81.8%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- TISSUB SPECIFICITY: UBICUITOUS.
-i- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                Blattella germanica (German cockroach).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota, Neoptera; Orthopterolidea; Dictyoptera; Blattarla;
Blabberoidea; Blattellidae; Blattellinae; Blattella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 164;
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  Indels
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                                                                                                                                                                                         164 AA
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81.8%; Pred. No. 0.011;
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(Rel. 21, Last sequence update)
(Rel. 38, Last annotation update)
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  Mismatches
                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyclosporin; Isomerase; Rotamase.
SEQUENCE 164 AA; 17935 MW; A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
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                                                                                                                                                                                                                                              (Rel. 34, Created)
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    Conservative
                                                                                                                                                                                                    STANDARD;
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47 GYKGSRFHRVI 57
                                           1 GYKNSKFHRVI 11
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                         79 GYKNSKFHHMI
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01-MAR-1992
15-JUL-1999
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                                                                                                                                                                                                                                              01-0CT-1996
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CYPB_CHICK
ID CYPB_C
AC P24367
DT 01-MAR
DT 15-JUL
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Sims M.;
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                                                                                                                                                                                                                                                                         between the Swiss Institute of Bloinformatics and the EMBL outstation. the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                               the secretory pathway.";
J. BALO. Chem. 266:10739-10742(1991).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICCHLUM LUMEN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
           (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
                                                                                                          MEDLINE-91250364; PubMed-2040593;
Caroni P., Rothenfluh A., McGlynn E., Schneider C.;
"S-cyclophilin. New member of the cyclophilin family associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PREVENT SECRETION FROM ER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
Multigene family.
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0
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0VT-1997 (Rel. 35, Last annotation update)
01-0VT-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLL CIS-TRANS ISOMERASE 11 (EC 5.2.1.8) (PPIASE)
ROTAMANE) (CYCLPHILIN-11).
CYP-11 OR T01B7.4.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%; Score 50; DB 1; Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D9C0C2E528E25B59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.022;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  Interpro: IPR002130; CSA_PPIBSE.
Pfam: PF00160; pro_isomerase; 1.
PRNTS: PR00153; CSAPPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1; IPROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
MEDLINE-96276416; PubMed-8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 AA; 22413 MW;
                                                                                                                                                                                                                                                                                                                                                                  EMBL; M63553; AAA49064.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match . 83.3
Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
207
207
                                                                                                                                                                                                                                                                                                                                                                               PIR; A40516; A40516.
HSSP; P23284; 1CYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GYKNSKFHRVI 11
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYPB_CAEEL
P52018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
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01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-1911493: PubMed=2408007;
Bergsma D.J., Sylvester D.;
"A Chinese hamster ovary cyclophilin cDNA sequence.";
"A Chinese hamster ovary cyclophilin cDNA sequence.";
"I Chinese hamster oxary cyclophilin cDNA sequence.";
"I CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEDITION: PPLASES ACCELERATE THE FOLDING OF PROLINE IMIDIC PEDITION IN OLIGORPEPTIDES.
"I CHAZYME REGULATION: BINDS CYCLOSPORIN A (CSA), CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITONY ACTION ON PPIASE.
"I SUBCELLULAR LOCATION: CYTOPLASMIC."
"I SUBCELLULAR LOCATION: CYTOPLASMIC."
"I SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
Page A.P., Macniven K., Hengartner M.O.;
flooning and biochemical characterization of the cyclophilin
homologues from the free-living nematode Caenorhabditis elegans.";
Biochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                          -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTULITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metázoa, Chordáta, Craniata, Vertebráta, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                             Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isomerase, Rotamase, Multigene family.
SEQUENCE 183 AA; 20193 MW; 23549C922828C533 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49; DB 1;
Pred. No. 0.03;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U34955; AAC47115.1; -.
EMBL; 266499; CAA91297.1; -.
HSSP; P05092; 3CYS.
WormPep; T01B7.4; CE03588.
InterPro; TPR002130; CSA_PPIASE,
Pfam; PP00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 81.7
Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AuG-1990 (Rel. 15, Created)
01-AuG-1990 (Rel. 15, Last sequence update)
15-DEC-1999 (Rel. 37, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN) (SP18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
-1- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6 X CBA; TISSUE-Thymus; MEDLINE-90326555; PubMed-2197604; Hasel K.W.; Sutcliffe J.G.; Nucleotide sequence of a cDNA coding for mouse cyclophilin."; Nucleic Acids Res. 18:4019-4019(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                              Score 48; DB 1; Length 163;
Pred. No. 0.041;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                            163 AA; 17768 MW; 02D44F71B8F87A1A CRC64;
                                                                                                                                                                                                                                                                                           Cyclosporin; Isomerase; Rotamase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 AA
                                                                                                                                            EMBL, X17105, CAA34961.1; -. PIR, S07597, CSHYAC. HASP, PO5092, 3CYY. InterPro; IPR002130, CSA_PPIASE. Pfam; PF00160; pro_isomerase; 1. PR0SITE; PS00170, CSA_PPIASE.. PROSITE; PS00172, CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-19; 21-27 AND 76-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Macrophage;
MEDLINE-92228816; PubMed-1565646;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GYKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 GYKGSSFHRII 56
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P17742;
                                                                                                                                                                                                                                                                                                            INIT_MET
SEQUENCE
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CYPH_MOUSE
     SO THE DRAW DOWN
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CYPH_RAT STANDARD; PRT: 163 AA.
P1011; P18303;
01-MAR-1989 (Rel. 10, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (RC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN) (P31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Connern C.P., Halestrap A.P.;
"Purification and N-terminal sequencing of peptidyl-prolyl cis-trans-
"spurification and N-terminal sequencing of peptidyl-prolyl cis-trans-
isomerase from rat liver mitochondrial matrix reveals the existence
of a distinct mitochondrial cyclophilin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Theodor L., Peleg D., Meyuhas O.; "P31, a mammalian housekeeping protein encoded by a multigene family containing a high proportion of pseudogenes."; Biophys. Acta 826:137-146(1985).
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
MEDLINE=88283345; PubMed=3293952;
Danielson P.E., Forss-Petter S., Brow M.A., Calavetta L.,
Douglass J., Milner R.J., Sutcliffe J.G.;
"PIBI5: a cDNA clone of the rat mRNA encoding cyclophilin.";
DNA 7:261-267(1988).
                                                                                                                                                                                                                                                                                 Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE-91232390; PubMed-1851525;
Lad R.P., Smith M.A., Hilt D.C.;
"Molecular cloning and regional distribution of rat brain
                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                  17 19 GRV -> TXP (IN REF. 2).
163 AA; 17840 MW; AC724D44DBBF4840 CRC64;
                                                                                                                                                                                       Cyclosporin; Isomerase; Rotamase; Multigene family.
                                                                                                                                                                                                                                                                               Score 48; DB 1;
Pred. No. 0.041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brain Res. Mol. Brain Res. 9:239-244(1991).
                                                                                                                                                                                                                                                                                                                 Mismatches
send an email to license@isb-sib.ch)
                                                                                                                       Pfam: PF00160; pro_isomerase; 1. PRNTMS; PR00153; CSAPPISMRASE. PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Liver;
MEDLINE-92287042; PubMed-1599421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SABRA;
MEDLINE-86026347; PubMed-2996604;
                                                                                        MGD; MGI:97749; Ppia.
InterPro; IPR002130; CSA_PPIase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                 80.08;
72.78;
                           EMBL; X52803; CAA36989.1; -. PIR; S10327; CSMSA.
                                                          HSSP; P05092; 3CYS.
SWISS-2DPAGE; P17742; MOUSE.
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                               1 CYKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                                                            46 GYKGSSFHRII 56
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cyclophilin."
                                             S10327
                                                                                                                                                                                                     INIT_MET
CONFLICT
                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                Matches
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CYPM_ART

ID CYPM_RAT

TO P29117;

DT 01-DEC-199

DT 01-DEC-199

DT 01-DEC-199

DT 01-DEC-199

DT 01-NOV-199

DE (EC 5.2.1.

GN RATIUS DOC

CE URARYODES

NAMMANIA 13.

OC RATIUS OC

NCBL TAXID WIS

RA Price N.T.

RA CONDET C.

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01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 5 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
              PINCHELO. 2 484:301-1930/1934.

-1. FUNCTION: PITASES ACCELERATE THE FOLDING OF PROTEINS.

-1. FUNCTION: PITASES ACCELERATE THE FOLDING OF PROTEINS.

-1. FUNCTION: DIAGOPEPTIDES.

-1. ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA), CSA MEDIATES SOME OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.

-1. SUBCELLUAR LOCATION: CYTOPLASMIC.

-1. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

-1. SIMILARITY: SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page A.P., Macniven K., Hengartner M.O.;
"Cloning and biochemical characterization of the cyclophilin
homologues from the free-living nematode Caenorhabditis elegans.";
Biochem. J. 317:179-185(1996).
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CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.0%; Score 48; DB 1; Length 163; 72.7%; Pred. No. 0.041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 AA; 17743 MW; DD16D1C980474414 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyclosporin; Isomerase; Rotamase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
MEDLINE-96276416: PubMed-8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A15632; CSRT31.
PIR; A29819; CSRTA.
HSSP: P05092; 3CYS.
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M19533; AAA41009.1; -. EMBL; M25637; AAB59719.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72.77
Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| | |||:|
46 GYKGSSFHRII 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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ID CYP5_CAEEL
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SEQUENCE
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SO THE STREET OF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Métazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CISTARANS ISOMERASE, MITOCHONDRIAL PRECURSOR
(EC. 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Price N.T., Woodfield K.Y., Halestrap A.P.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                        InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1,
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS000170; CSA_PPIASE_1; 1.
PROSITE; PS00072; CSA_PPIASE_2; 1.
Isomerase; Rocumase; Multigene family.
SEQUENCE 204 AA; 22366 MW; 22ABB39AD1127BAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 1;
Pred. No. 0.052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.05
); Mismatches
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HSSP; P05092; 3CYS.
InterPro; IPR002130; CSA_PPIase.
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PRINTS; PR00153; CSAPPISMRASE.
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01-NOV-1997 (Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%;
81.8%;
                                                                                                                                        EMBL; U31948; AAC47126.1; -. HSSP; P23284; 1CYN.
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MEDLINE-92078192: PubMed-1744118;

MEDLINE-92078192: PubMed-1744118;

A REDLINE-92078192: PubMed-1744118;

A Appelbaum E., Cusimano D., Livi G.P., McLauglin M.M., Kasyan K., Sapelbaum E., Cusimano D., Livi G.P., McLauglin M.M., Kasyan K., Porter T.G., Silverman C., Dunnington D., Hand A., Prichett W.P., A Bossard M.J., Brandt M., Levy M.A.; Peptidyl-prolyl isomerases.

The cyclophilin multigene family of peptidyl-prolyl isomerases.

Characterization of three separate human isoforms.";

L. J. Biol. Chem. 266:32204-33214(1991).

-: FUNCTION: PITASES ACCERRATE THE FOLDING OF PROLINE IMIDIC C. I- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.

-: SUBLIARITY: BELONGS TO THE CYCLOPHILIN TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                               Gaps
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
Cyclosporin; Isomerase; Rotamase; Multigene family; Mitochondrion;
Transit peptide.

1 29 MITOCHONDRION.
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Pfam: PF00160; pro_isomerase; 1.
PRINTS; PR00151; CSA_PPIASE.
PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
Transit peptide.

MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR
(EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
PPIF OR CYP3.
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID-9606;
                                                                                     PEPTIDYL-PROLYL CIS-TRANS ISOMERASE. MISSING (IN A MINOR FORM).

S -> R.

C -> A (IN REF. 2).
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PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
D7C76F1D4049F16A CRC64;
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                                                                                                                                                                                                             Score 48; DB 1; Length 206;
Pred. No. 0.053;
0; Mismatches 2; Indels
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-> A (IN REF. 2).
69048482631B9FAD CRC64;
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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206 AA;
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88 GYKGSTFHRVI 98
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AC P30405;
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Search completed: January 15, 2002, 13:14:59 Job time: 655 sec

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January 15, 2002, 13:16:25 ; Search time 78.85 Seconds (without alignments) 20.406 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

OQUHHHHHHXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	001490 001490 001490 001490 001490 001490 001490 001490 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC (CYCLOPHILIN B) (ROTAMASE). CYPHIOMYCES SP. PC-2. ELMATYOLS FUNG1: Chytridiomycota; Neocallimasticaceae; Orpinomyces. NCBL_TAX_LD-50059; [1] NCBL_TAX_LD-50059; [2] NCBL_TAX_LD-50059; [3] SEQUENCE FROM N.A., AND SEQUENCE OF 23-52. MEDLINE-5723986; PubMed-7708690; Chen H., Li XL., Ljungdahl L.G.; "A cyclophilin from the polycentric anaerobic rumen sp. strain pc-2 is highly homologous to vertebrate of the control of the polycentric anaerobic rumen sp. strain pc-2 is highly homologous to vertebrate of the control of the process of the control of the process of the control of the process of the process of the process of the process of the control of the process of the pr	PRELIMINARY; 998 (TrEMBLrel. 909 (TrEMBLrel. 101 (TrEMBLrel. PROLYL CIS-TRAN ILIN B) (ROTAMAS CES SP. PC-2. 13; Fungi; Chytri masticaceae; Orp ID-50059; PROM N.A., AND 95223986; PubMed Li XL., Ljung ARITY: BELONGS POOLOS 1 1 1 2 2 2 2 2 2 2 2 2 3 2 3 2 3 2 3 2	MBLrel. 08, Crea MBLrel. 08, Last MBLrel. 17, Last CIS-TRANS ISOMER (ROTAMASE). PC-2. CDYLTIGIOMYCCOT CONTROL OF CONTROL CONTROL CONTROL OF C	PRELIMINARY; PRT; 203 AA. 90, 0V-1998 (TEMBLrel. 08, Created) OV-1998 (TEMBLrel. 10, Last sequence update) OV-1998 (TEMBLrel. 17 Last sequence update) LOPHILIN B) (ROTAMASE). IDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (STRONG). LOPHILIN B) (ROTAMASE). INCOMES SD. PC-2. INCOMES SD. PC-2. INCOMES INCOMEDIATION OF STRONG	203 AA. luence up lotation B PRECURN 23-52. 23-52. 7-2591(1) FFOLDING OMERIZAT C (CSA) I C (CS	5.2.1.8 fungus yclophi rEINS. ROLINE CYPB. SYSE FAMI) (PPIASE) Orpinomyces lin B."; IMIDIC IMILARITY). LY.
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	ENCE	AA;	21969 MW;		SECRE TY). 94305		

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216 AA; 23742 MW; 2D0410A07AA9E420 CRC64;
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Matches 11; Conserv
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN B (EC 5.2.1.8).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                              Gaps
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-i- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-i- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERAES FAMILY.
FRANS ISOMERAES FAMILY.
HSSP; P23284; 1CYN.
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NCBI_TaxID=9606;
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                    100.0%; Score 60; DB 3; Length 203; 100.0%; Pred. No. 0.0019; ive 0; Mismatches 0; Indels
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TISSUE-SKIN, AND MELANOMA;
Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; BC001125; AAH01125.1; -.
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=WISTAR-KYOTO; TISSUE-KIDNEY;
KAINET D.B., Doris P.A.;
"Cyclophilin B.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22802 MW; 02408DFA7157218C CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B).
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InterPro; IPR002130; CSA_PPIase.
                                            Conservative
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Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishil Y., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishil Y., A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishil Y., A Takawa T., Hara M., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Lawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Shaburner M., Batalov S., Casawant T., Radota K., Matsuda H.A., Saito T., Gissi C., King B., Kochiwa H., As Fleischmann W., Casaterland T., Gissi C., King B., Kochiwa H., Sati M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T., Rasai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fullica M., Gariboldi M., Brownstein M.J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Asasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-Oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Mynshay-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AKO02357: BAB22036.1;
MGD; MGI:97750; Ppib.
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   Length 216;
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100.0%; Score 60; DB 4; L
11arity 100.0%; Pred. No. 0.002;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 AA.
                                                                                                                                                                                                                                                                                                                                                                           216 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q98UES PRELLMINARY; PRT;
Q98UES;
01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PSS0072; CSA_PPIASE_2; 1
SEQUENCE 216 AA; 23713 MW; CEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, PEPTIDYLPROLYL ISOMERASE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
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us-09-720-469-4.rspt

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Andana Manatides P. G. Scherer S.E., Li P.W., Hoshins R.A., Goleyne J.D.,
R.A. Addans Manatides D.G., Scherer S.E., Li P.W., Hoshins R.A., Galle R.F.,
R. Burdatides D.G., Scherer S.E., Li P.W., Hoshins R.A., Galle R.F.,
R. Brandan R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R.A. Amatalides D. Baxter E.G., Helt G., Champe M., Pfeiffer B.D.,
R.A. Andans M.A. Basul A., An H.-J., Andrews-Pfannach. C., Baldwin D.,
Ballew R.M., Basul A., Barman B.P., Bardario D., Bolshakov S.,
Ballew R.M., Basul A., Barman B.P., Bhandari D., Bolshakov S.,
Burkova D., Butchan M.R., Bouw Y., Borns B.P., Bardiar P., Brandria T.,
R.A. Gawley S., Dalike C., Davenport L.B., Davies P.,
R.A. Chandra D.A., Cavil B.S., Dalike C., Davenport L.B., Davies P.,
R.A. Challes B., Delcher A., Dabeng Z., Mays A.D., Dew I., Diez S.M.,
Durbin K.J. Evangalista C.C., Ferraz C., Ferraz 
                                                                                                                                                                                                               Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOLDING OF PROTEINS (BY SIMILARITY).
                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                    MEDLINE=20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE003458; AAF46873.1; -. HSSP; P23284; 1CYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0034753; CG2852
                               PRELIMINARY;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                 STRAIN-BERKELEY;
                                                                                                                                   CG2852 PROTEIN.
                                                                    01-MAY-2000
01-MAY-2000
                                                      09W227
                               09W227
                                                                                                                                                   CG2852
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                                                                                                                                                                            SEQUENCE FROM N.A.
Amano T., Yoshizato K.;
Isolation of genes involved in intestinal remodeling during anuran metamorphosis.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF170328; AAK11503.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Last Sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C1709.04C (EC 5.2.1.8).
SPBC1709.04C.
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERARE B (FRAGMENT).
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                      90.0%; Score 54; DB 13; Length 104; 90.9%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 3; Length 173;
Pred. No. 0.031;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                              11350 MW; 8F6ADICD1C2FB3E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ນ1 protein; Isomerase: Rotamase.
173 AA; 18905 MW; 116DA3AF5FEDບບໍຣິຣ5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.0
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                        Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                              104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYKNSKFHRVI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GYKNSKFHRVI 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998
                                                                                                                                                                                                                                                                                                             Somerase.
                                                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
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074729; 074729 φ

RESULT 074729

qq ð

Isomerase; Rotamase.
SEQUENCE 205 AA; 22199 MW; A9CEF88BICC813F7 CRC64; PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.

54

ò a RESULT

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MEDLINE-96123383; PubMed*8577319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P05092; 1CWL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Q9XZZ5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-FCCI/HN;
Li X.R., Yu X.B., Luo S.H., Shan Z.X., Fang J.M., Xu J.;
Li X.R., Yu X.B., Luo S.H., Shan Z.X., Fang J.M., Xu J.;
Sequence of cyclophilin (cyppfl) gene of Plasmodium falciparum
"Sequence of cyclophilin (cyppfl) gene of Plasmodium falciparum
(isolate FCCI/HN).";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
FOLDING OF PROTEINS (BY SIMILARITY).
-! CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
-! SIMILARITY: BELOMOS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
TRANS ISOMERASE FAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROIYL CIS-TRANS ISOMERASE PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
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Plasmodium falciparum (isolate Dd2), and
Plasmodium falciparum (isolate hb3).
Bukaryotam falciparum (isolate hb3).
Eukaryota Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329, 57267, 137071;
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.0%; Score 51; DB 5; Length 210; 81.8%; Pred. No. 0.089; 1; Mismatches 1; Indels
Score 53; DB 5; Length 205;
Pred. No. 0.037;
                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 AA; 24049 MW; 778A31CE0FD47D26 CRC64;
                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                       210 AA
                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam: PF00160; pro_isomerase: 1.
PRINTS: PR00153; CSAPPISNRASE: 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1999 (TrEMBLrel. 09, Created)
                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                       PRT;
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InterPro; IPR002130; CSA_PPIase,
InterPro; IPR002114; PTS_HPr_ser.
  88.3%;
81.8%;
                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, CYCLOPHILIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 85.0
Best Local Similarity 81.8
Matches 9; Conservative
    Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rotamase.
                                                                                      1 GYKNSKFHRVI 11
                                                                                                            ||| ||||||||||| 72 GYKGSKFHRII 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYKNSKFHRVI 11
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89 GYKNTTFHRVI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isomerase;
SEQUENCE
                                                                                                                                                                                                                                       209060
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Gaps
Reddy G.R.; "Cloning and characterization of a Plasmodium falciparum cyclophilin gene that is stage-specifically expressed."; Mol. Biochem. Parasitol, 73:111-122(1995).
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-!- FUNCTION: PEPTIOYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALVITC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.
-- FEMBL; AJ288310; CAB41016.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lumbricus rubellus (Humus earthworm).
Bukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
Lumbricina; Lumbricidae; Lumbricus.
NCBI_TaxID=35632;
                                                                                                                         SEQUENCE FROM N.A.
MEDDILNE-84052193; Pubmed-8234327;
REDDI S.R., Chakrabarti D., Schuster S.M., Ferl R.J., Almira E.C., Dame J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malaria; Cyclosporin; Isomerase; Rotamase; Signal.
SIGNAL 1 39 POTENTIAL.
CHAIN 40 210 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Sturzenbaum S.R., Morgan A.J., Kille P.;
"isolated from earthworms exposed to Cd-supplemented artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51; DB 5; Length 210;
Pred. No. 0.089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSA (POTENTIAL).
778A359F0FD47D26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN A (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002130; CSA_PPHase.
InterPro; IPR002114; PTS_HPr_ser.
Pfam; PF00160; Pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMASE_1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS0072; CSA_PPIASE_2; 1.
PROSITE; PS00589; PTS_HPR_SER, UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 163 C
210 AA; 24049 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.0%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U10322; AAC46975.1;
HSSP; P05092; 2CPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
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Haing Y -1.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M.,
Hsing Y -1.C., Shaw J.-F.;
Chen C.-S., Shaw J.-F.;
Characativa PAC P0035010 genomics sequence, complete sequence.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ACG73405; AAG03106.1;
EMBL, ACG73405; AAG03106.1;
FinterPro: IPR002130; CSA_PPISS.
Pfam; PF00160; Dro_Lsomerase; I.
PRINTS; PR00153; CSA_PPISRESE.
PROSITE; PS0072; CSA_PPISRESE.
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:97749; Ppia.
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%;
ilarity 72.7%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 39
39 AA; 4324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 GYKGSSFHRVI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GYKNSKFHRVI 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
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Q9ERB9;
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09R137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
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ID Q9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9FW22;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO ARABIDOPSIS THALIANA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (P34791) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hirudo medicinalis (Medicinal leech).
Eukaryota: Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida: Hirudiniformes; Hirudinidae; Hirudo.
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                                                                                                                                                                                                                                83.3%; Score 50; DB 5; Length 164; 81.8%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 5; Length 143;
Pred. No. 0.14;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                           164 AA; 17599 MW; B30D22D660966AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isomerase; Rotamase.
SEQUENCE 143 AA; 15398 MW; 64FFD82018480A6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN-A (EC 5.2.1.8).
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                                                                                                                                                                                                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR002130; CSA_PPIase.
Pfam: PF00160; pro_isomerase: 1.
PROSITE; PR00153; CSAPPIASE_1: 1.
PROSITE; PS50072; CSA_PPIASE_1: 1.
PROSITE; PS50072; CSA_PPIASE_2: 1.
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81.8%;
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Best Local Similarity 81.8°
'.e 9; Conservative
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                                                                                                                 Isomerase; Rotamase.
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                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                           SEQUENCE
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09FW22

1D 09FW22

AC 09FW22,

DT 01-MAR:

DT 01-JWAR:

DF 01-JWAR:

DF 01-JWAR:

DF 01-JWAR:

DF 01-JWAR:

DF 07-JWAR:

DF 
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025093
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DT 01-NO
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                                                                                                                             Gaps
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"Haploinsufficient growth defects, increased Th2 cytokine production and cyclosporine resistance in mice lacking CYPA.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, AF171073; AAD50996.1; -.
HSSP; P05092; 2CPL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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0
                                                                         Score 49; DB 10; Length 173; Pred. No. 0.17;
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Pred. No. 0.059;
                                                                                                                             Indels
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173 AA; 19158 MW; 28EADE80F4625EB9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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"Isolation of a cDNA sequence encoding a peptidy1-proly1 cis-trans isomerase from Periplaneta americana antennae.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- PUNCTION: PEPTIDV1-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
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01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-JUN-2001 (TrEMBLrel, 17, Last annotation update)
PEPTIDYL-PROLYL ISTANS ISOMERASE (FRAGMENT).
Periplaneta americana (American cockroach).
Periplaneta americana (American cockroach).
Periplaneta americana (Anthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
MCBL_TaxID-6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 48; DB 11; Length 70; 72.7%; Pred. No. 0.11; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 70 70 70 70 AA; 7841 MW; 472374C12B7ACEC9 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                             (Golden hamster).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF00160; pro_isomerase; 1. PROUNTS; CAPPITSMRASE. PROSTIE; PS00170; CSA_PPIASE_1; PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002130; CSA_PPIase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF041412; AAD56049.1; -.
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Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                             CYCLOPHILIN (FRAGMENT)
                                                                Mesocricetus auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYKNSKFHRVI 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P05092; 2CPL.
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                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-ANTENNAE;
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NON_TER
SEQUENCE
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Q9UBK2;
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Q9UBK2
     DDE BERRY NAME OF STATE OF STA
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                                             Length 78;
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 DB 5;
                                             Score 48; DB 5
Pred. No. 0.12;
0; Mismatches
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                                                                                                                                         Search completed: January 15, 2002, 13:16:26 Job time: 657 sec
                                             80.0%;
81.8%;
                                                                 9; Conservative
                                                                                   1 GYKNSKFHRVI 11
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Best Local Similarity
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GenCore version 4.5
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OM protein . protein search, using sw model

January 15, 2002, 13:05:28 ; Search time 81.32 Seconds (without alignments) 10.020 Million cell updates/sec Run on:

US-09-720-469-5 71

1 NFKLKHYGPGW 11 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 seqs, 74073290 residues Searched:

522463 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summarles Post-processing: Minimum Match 0%

Database :

A_Geneseq_1101:*

1. SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2. SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human cyclophilin	Human secreted pro	Human cyclophilin	Human cyclophilin	Human cancer assoc	Cyclophilin C. Mu	Human cyclophilin	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	
OI .	AAY69925	AAG00090	AAB73302	AAB73301	AAB43878	AAR32353	AAY69947	AAG18027	AAG08983	AAG08982	AAG08981
BC :	21	21	22	22	21	14	21	21	21	21	21
Query Match Length DB	11	166	211	216	291	212	10	125	152	204	218
Query	100.0	100.0	100.0	100.0	100.0	85.9	83.1	73.2	73.2	73.2	73.2
Score	7.1	71	71	71	7.1	61	59	52	52	52	52
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Claim 4; Page 50; 64pp; Japanese.

Arabidopsis thalia	is	is	is	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Ø	Ø	Human cyclophilin	Human cyclophilin	Arabidopsis thalia		Arabidopsis thalia	Ø	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Human colon cancer	Gene 14 human secr	Human secreted pro	æ	Breast cancer-asso	Breast cancer-asso	Breast cancer-asso	Porcine peptidyl-p	Porcine peptidyl p	Porcine peptidyl p	oph <u>i</u> li	Cyclophilin, Homo	Calcineurin protei	Human cyclophilin	Human breast cance	Gene 22 human secr
AAG18026	AAG18025	AAG44157	AAG44156	AAG44155	AAG29380	AAG29379	AAG05073	AAG05072	AAU01197	AAY69928	AAG15070	AAG48166	AAG15069	AAG48165	AAG16463	AAG16462	AAG16461	AAG76091	AAB64736	AAB64737	AAW44366	AAB98718	AAW44367	AAB98719	AAR10763	AAR72917	AAR72961	AAR13726	AAP90431	AAW56028	AAU01195	AAB98722	AAB51902
21	21	21	21	21	21	21	21	21	22	21	21	21	21	21	21	21	21	22	22	22	19	22	19	22	12	16	16	12	10	19	22	22	21
228	236	162	176	186	201	218	254	259	207	σ	191	192	205	206	252	254	260	82	114	114	121	121	141	141	145	4	4	9	9	9	165	9	0
73.2	73.2	71.8	71.8	71.8	71.8	71.8	66.2	66.2	64.8	63.4	63.4	63.4	63.4	63.4	63.4	63.4	63.4	9.09	9.09	9.09	9.09	9.09	9.09	9.09	9.09	9.09	9.09	9.09			9.09		
52	25	51	51	21	51	21	47	47	46	45	45	42	45	45	45	45	45	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43
12	13	14	15	16	17	18	19	20	21	22	23	24	25	36	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Tumour antigen peptides derived from cyclophilin B for treatment and diagnosis of tumours -Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy. Human cyclophilin B peptide fragment #5. AAY69925 standard; peptide; 11 AA (SUMU) SUMITOMO PHARM CO LID. 98JP-0178449. 99WO-JP03360 11-APR-2000 (first entry) WPI; 2000-116932/10. Gomi S; (ITOH/) ITOH K. WO9967288-A1. 24-JUN-1999; 25-JUN-1998; Homo sapiens 29-DEC-1999. AAY69925; Itoh K, AAY69925

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Gaps

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Indels

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Mismatches

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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic
               This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mapping procedures. They are used to obtain upstream sequences and to design expression and secretion vectors.
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                                                                                                                                                              Score 71; DB 21; Length 11; Pred. No. 9e-06;
                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein, SEQ ID NO: 4171.
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100.0%;
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Best Local Similarity
Matches 11; Conserv
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Score 71; DB 21; Length 166; Pred. No. 0.00014;

100.0%; 100.0%;

Query Match Best Local Similarity

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The invention relates to a composition for modulating somatolactogenic function, comprising cyclophilin B (CypB), a mutant of cyclophilin B (particularly a CypB mutant in which residues 2-12 of the mature protein are absent) or an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone (e.g., prolactin, growth hormone). The Invention also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and method for diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic functions useful for augmenting somatolactogenic functions useful for augmenting somatolactogenic function in the animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyclophilin B mutent or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, is useful for inhibiting somatolactogenic function in the animal. A composition comprising cyclophilin B is useful in the treatment of immunosuppression, in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, is useful for treating HIV infection, breast and prostate cancer, glgantism/acromegaly, and hyperprolactineemia. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represents a human cyclophilin B C-terminal mutant, CypB-AIAKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone .
                                                                                                                                                                                                                                                                                                                        Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis, HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia; C-terminal deletion mutant; mutein.
                                                                                                                                                                                                                                                                                      Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.
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Pred. No. 0.00018;
                                                                                                                                                     AAB73302 standard; protein; 211 AA.
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                         .127 nfklkhygpgw 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, is useful for inhibiting somatolactogenic function in the animal. A composition comprising cyclophilin B is useful in the treatment of immunosupression, in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, is useful for treating HIV infection, breast and prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature; muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia.
      Gaps
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      Indels
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11; Conservative
                                                                                             127 nfklkhygpgw 137
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Matches
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include: Cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antialeragic; antidathritic; antidiabetic; antiasthmatic; antialeragic; antibacterial; antiviral; dermatcological; neuroprotective; cardiant; thrombolytic; coaquiant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune disorders, alleragic reactions, graft versus host disease and organ effection, modulate haemostatic or thrombolytic activity, modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                     diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antidiflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
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                                                                                                                                                                                                                                                                                                     Human; cancer associated gene; cancer antigen; detection; cancer;
                                                                                                                                                                                                                                                             Human cancer associated protein sequence SEQ ID NO:1323.
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                                                                                                                            AAB43878 standard; Protein; 291 AA.
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WPI; 2000-587533/55.
N-PSDB; AAC78087.
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                                                                                                                                                                       AAB43878;
                  127
                                                                                                       AAB43878
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291 AA;

Sequence

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Gaps

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22; Length 216; Indels

100.0%; Score 71; DB 22; 100.0%; Pred. No. 0.00018; ive 0; Mismatches 0;

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Homo sapiens
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Best Local Si
Matches 9;
                                                                                                       AAY69947;
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                                                  AAY69947
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according to this cDNA was isolated from a substracted stronal cell line
according to the stronal cell line with interleukin-
according to the stronal cell interleukin-
according to the stronal strong to the strong to the strong to the strong cell cell of the strong to the strong cell of the strong cell intercell the strong to the strong cell of cyclosporin action for the strong to the strong cell intercell interpretation of the strong cell cell interpretation of the strong cell interpretation of the strong cell interpretation of the strong cell interpretation of the strong cell cell interpretation of the strong cell cell interpretation of the strong cell interpretation of the strong cell cell interpretation of the strong cell interpretation of the strong c
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                                  Gaps
                                                                                                                                                                                                                                                                                                                              Cyclophilin C; bone marrow; stromal cell line; AC 6; interleukin-1; IL-1; cyp A; cyp B; peptidyl-prolyl isomerase; PPIase; cyclosporin A; CsA; ligand; calcineurin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclophilin C polypeptide and nucleic acid encoding it - useful for screening a tissue-specific immunosuppressive agent
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Pred. No. 0.0088;
0; Mismatches 1; Indels
                                Indels
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                Pred. No. 0.00024;
                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                        AAR32353 standard; Protein; 212 AA.
100.08;
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90.9%;
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                                11; Conservative
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202 nfklkhygpgw 212
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                                                                  1 NFKLKHYGPGW 11
                Best Local Similarity
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                               Cyclophilin C.
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
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121

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1 NFKLKHYGPGW 11

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour antigen peptides derived from cyclophilin B for treatment and
                                                                                                                                                              Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy.
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                                                                                                                       Human cyclophilin B peptide fragment #27
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AAY69947 ştandard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                      98JP-0178449.
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es 9; Conser
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990S-0140354.
990S-0140695.
990S-0140823.
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99US-0130449.
99US-0130510.
99US-0130891.
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99US-0132048.
99US-0132407.
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99US-0132485.
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99US-0134256.
99US-0134218.
99US-0134219.
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99US-0135353.
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99US-0137724.
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99US-0139750.
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99US-0134768
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99US-0136021
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99US-0136782
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99US-0137528
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99US-0138847
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99US-0143542
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99US-0144086
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21-APR-1999

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24-APR-1999

30-APR-1999

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16-JUL-1999;
16-JUL-1999;
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23-JUN-1999;
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09-JUL-1999;
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13-JUL-1999;
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Pred. No. 0.17
1; Mismatches
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                                                                                                 9905-0159294
9905-0159294
9905-01593295
9905-0159330
9905-0159331
9905-0159638
9905-0159638
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9905-0160767
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990S-0161360.
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990S-0123180.
990S-0123548.
990S-0125788.
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Best Local Similarity 81.8%;
Matches 9; Conservative
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46 nfklkhtgpgf 56
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
28 - SEP - 1999, 29 - SEP - 1999, 05 - OCT - 1999, 06 - OCT - 1999, 07 - OCT - 1999, 13 - OCT - 1999, 13 - OCT - 1999, 14 - OCT - 1999, 16 - OCT - 1999, 17 - OCT - 1999, 18 - OCT - 1999, 18 - OCT - 1999, 25 - OCT - 1999, 26 - OCT - 1999, 26 - OCT - 1999, 26 - OCT - 1999, 27 - OCT - 1999, 27 - OCT - 1999, 28 - OCT - 1990, 28 - O
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 0.21;
1; Mismatches 1; Indala
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illarity 81.8%;
Conservative 1
                                         990S - 0159295
990S - 0159329
990S - 0159330
990S - 0159331
990S - 0159538
990S - 0159588
990S - 0160741
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99US-0161405.
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99US-0161359.
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99US-0161361.
99US-0161920.
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99US-0123180.
99US-012348.
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99US-0126785.
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99US-0160989.
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99US-0161993.
99US-0162142.
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Matches 9; Conserv
    12 - OCT - 1999;

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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23-JUN-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Best Local Similarity 81.8
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Search completed: January 15, 2002, 13:05:28
Job time: 199 sec

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Sequence 10, Application US/08482728A

Patent No. 5968802

GENERAL INFORMATION:

APPLICANT: Player, Joseph
APPLICANT: Player, Joseph
APPLICANT: Payan, Donald
TILE OF INVENTION: No. 5968802el Nuclear Cyclophilin
MUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco
STATE: California
COUNTRY: United States
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
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COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLLASSIFICATION: 07-JUN-1995
ATTORNBY/AGENT INFORMATION:
NAME: Silva, Robin M.
REFERENCE/POCKET NUMBER: 34.30
TELEPONE: (415) 781-1989
TELEPONE: (415) 781-1989
TELEPRIN: (415) 398-3249
INFORMATION FOR IND O: 10:
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                         1 NFKLKHYGPGW 11
                                                                                                                                                                                                                                                          US-09-720-469-5
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Query
Match Length DB
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                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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                                                                                                                                                            GO:
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Gaps

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Length 126;

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ADDRESSEE: Flehr, Hobbach, Test, Albritton
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                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Friedman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08482728A
Patent No. 5968802
GENERAL INPORMATION:
APPLICANT: Wang Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08,005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION NUMBER: 08,07/740,375
PRIOR APPLICATION NUMBER: 08,07/740,375
FILING DATE: 05-MG-1991
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 54,90A-92-1
TELEPHONE: 415-326-240
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH 1208 emino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5490A-92-1
                                                                                          RESULT 2
US-08-142-897-7
; Sequence 7, Application US/08142897
; Patent No. 5447852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.

Best Local Similarity 100.

Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-142-897-7
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        70 NFKLKHYGPGW 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-08-482-728A-11
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RESULT 4
US-08-142-897-5
Sequence 5, Application US/08142897
Fatent No. 547852
GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
TITLE OF INVENTION: No. 5447852el Cyclophiling, Associating Proteins
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
CORRESSOURCES: 10
CORRESSOURCE ADDRESS:
ADDRESSEE Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 0.0024;
                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
NAMME: S112A ROBIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
E: 8 Herbert
Four Embarcadero Center, Sulte 3400
          CITY: San Francisco
STATE: Callifornia
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
SOFTWARE: PATEM: PC-DOS/MS-DOS
SOFTWARE: PATEM: Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,895
                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEEX: 910 277299
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.98;
90.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 126 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 85.9
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-482-728A-11
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80.08;

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Best Local Similarity 80.0 Matches 8; Conservative
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Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Falser, Joseph
APPLICANT: Falser, Son Entry, Hobbach, Test, Albritton
ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: Flehr, Hobbach
ADDRESSEE: Galfornia
COUNTRY: United States

ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61; DB 1; Length 212;
Pred. No. 0.0039;
0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATONREY AGENT INFORMATION:
NAME: S11va, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 3-6,30/DJB/RMS
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEX: 910 277299
                                                                                                                          NAME: Dunn, Tracy D.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECHONE: 415-326-2420
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
INFORMATION FOR S
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.9%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 85.9
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-142-897-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 NFKLKHYGIGW 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NFKLKHYGPGW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: unk
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64.8%; Score 46; DB 2; Length 126;

Query Match

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Sequence 15, Application US/08451747

Sequence 15, Application US/08451747

Patent No. SB1107

APPLICANT: CARLOW, CLOTILDE K.S.

APPLICANT: PAGE, ANTON:

TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC

TITLE OF INVENTION: COMPOUNDS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
                                                                                                                                                                         US-08-145-995A-15
Sequence 15, Application US/08145995A
Patent No. 5482850
GENERAL N. FAR2880
GENERAL N. FARLOW. CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 1; Length 109;
Pred. No. 1.5;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPRATIES YSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
                     Mismatches
Pred. No. 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3440
TELEX: 200291 STR USTREEM: (117) 523-53 6440
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 130 WATER STREET CITY: BOSTON STATE: MASSACHUSETTS COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 109 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-145-995A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                     1 NFKLKHYGPG 10
                                                                                 11 ||| |||
70 NFTLKHVGPG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NFKLKHYGPG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02109
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,639
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REPERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
                     US 08/145,995
                                                                                                                   REFERENCE, DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELERA: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-08-658-658-013,
Sequence 13, Application US/08658639
patent No. 5914238
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/14
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAMME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                                                                                                                                                                                                  62.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 121 amino acids IYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-09-134-852-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-658-639-13
                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NFKLKHYGPG 10
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39 NFKEKHTGPG 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02110
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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ADDRESSEE: GRECORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-134-852-15
Sequence 15, Application US/09134852
Sequence 15, Application US/09134852
Sequence 15, Application US/09134852
GENERAL INFORMATION:
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADAID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.0%; Score 44; DB 2; Length 109; B0.0%; Pred. No. 1.5;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALEONETH Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred, No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-451-747-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: BOSTON
STATE: MASSACHUSETTS
                                              CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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CLASSIFICATION:
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                                                                                                        01915
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Gaps
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APPLICANT: KEESEE, SUSAN
APPLICANT: W. YING-JYE
APPLICANT: WJ. YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
Score 44; DB 3; · Length 109;
Pred. No. 1:5;
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; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-482-728A-9
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NFKLKHYGPG 10
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02110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-658-639-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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APPLICANT: OBAR, ROBERT
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
                   DB 2; Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                  2; Indels
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21
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CURLENT PELICATION NUMBER: US/08/944,604
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTP-021 (8395/24)
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Pred. No. 2.4;
                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
               60.6%; Score 43;
80.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08482728A Patent No. 5968802
                                                                                                                                                                                               Sequence 13, Application US/08944604 Patent No. 6218131 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-(
TELECOMMUNICATION INFORMATION:
TELEFHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.68;
80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Fisher, Joseph
ATILE OF INVENTION: No. 596
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.6
Best Local Similarity 80.0
Matches 8; Conservative
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-944-604-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                 1 NFKLKHYGPG 10
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26 NFILKHTGPG 35
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CITY: Boston
STATE: MA
COUNTRY: USA
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US-08-482-728A-9
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Gaps
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Patent No. 5914238
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KESSEC, SUSAN
APPLICANT: WU, YING-UYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 2; Length 127;
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUBER: US/08/482,728A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: 6 Herbert
ADDRESSEE: 6 Herbert
Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                     ATTORREY/ACENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REEFERENCE/DOOKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Testa, Hurwitz & Thibeault 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/658,639 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.6%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 amino acids
                                                                                                                    STATE: California
COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 60.6
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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us-09-720-469-5.rai

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APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: CARLOW, CHOPILDE K.S.
APPLICANT: CARLOW, COMPOUNDS
TITLE OF INVENTION: WETHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF ENVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 163;
                                                                                                                                                                                                                                                                                                                              E: Tracy J. Dunn
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.6%; Score 43; DB 1;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY AGENT INFORMATION:
RECISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                      RESULT 14
US-08-142-897-8
'Sequence 8, Application US/08142897
'Patent No. 5447852
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 163 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 60.6
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                               STREET: One Market Pl.
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) MOLECULE TYPE: protein US-08-142-897-8
        linea
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ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-08-145-995A-9
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                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: REESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-TYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
STREET: MA
COUNTRY: USA
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Pred. No. 2.8;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/944,604
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFRAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATORNEY AGENT INFORMATION:
NAME: MBYERS, THOMAG.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELEPOMMUNICATION INFORMATION:
TELEPAX: (617) 248-7000
TELEFAX: (617) 248-7100
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYRED: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08944604
Patent No. 6218131
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       60.6%;
80.0%;
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-944-604-14
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Best Local Similarity
Matches 8; Conserv
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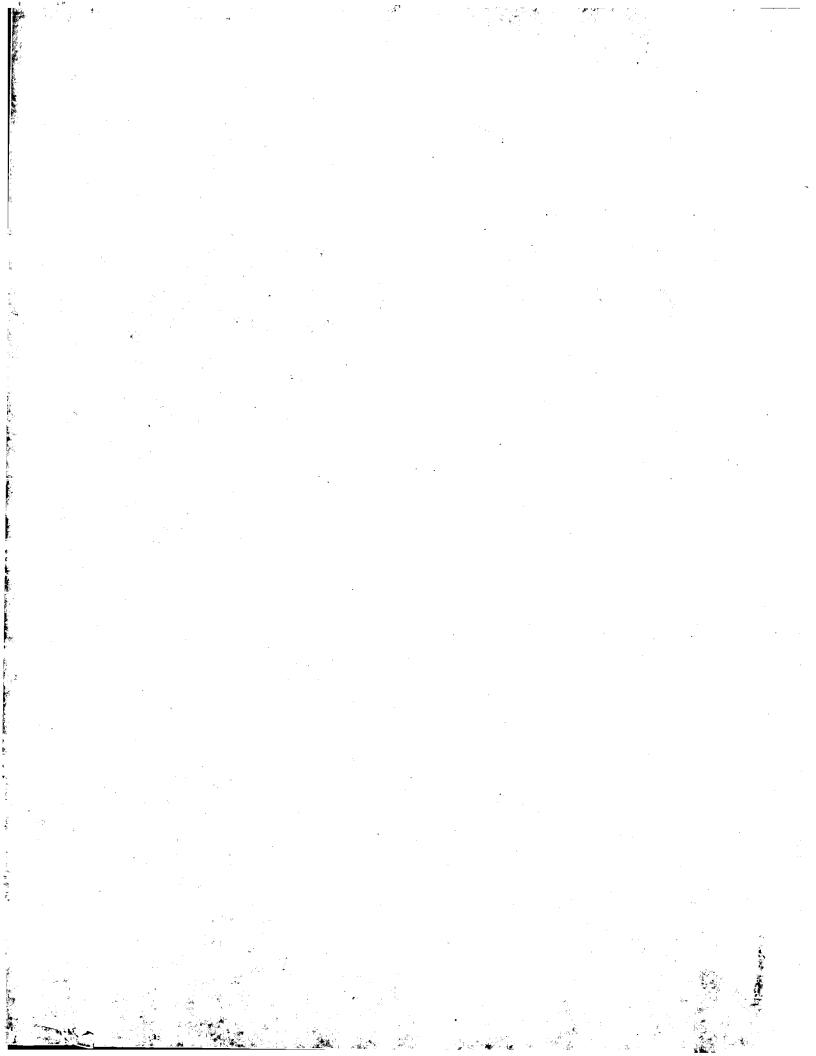
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60.6%; Score 43; DB 1; Length 164;
Best Local Similarity 80.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 2; Indels
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHWAN STREET: 130 WATER STREET
                                                    STREET: 130 WALEN COUNTRY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: 02109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NG-DOS
SOFTWARE: PALENTION DATA:
APPLICATION NUMBER: U5/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION NUMBER: 44406
FILING DATE: 34235
ATTORNEY AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 44406
TELEPHONE: (617) 523-3400
TELEPHONE: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SED ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPEE : amino acids
STRANDEDNESS: unknown
US-08-145-995A-9
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Search completed: January 15, 2002, 13:03:59 Job time: 215 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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January 15, 2002, 13:06:15; search time 42.04 seconds (without alignments) 19:931 Million cell updates/sec Run on:

US-09-720-469-5 Title: Perfect score:

1 NFKLKHYGPGW 11 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	peptidylprolyl so	_				peptidylprolyl iso		_	_			_			, 1	dylprolyl		pentidylprolyliso	-		. –	ء ،	rolvi	+	peptidylprolyl 180				
·	ID	S71547	A40516	CSHUB	A56861	T18573	T21587	A40047	A54204	T50838	T49204	T50767	T47724	T50837	T02489	833212	S48018	T18578	863995	868767	A41581	T27034	T52479	B53422	B82777	T27371	T27882	T27373	CSBOAB	CSPGA
	y h Length DB	183	207	208		.4 201 2		9 212	9 212	2 204	234	8 176	8 176	8 201		573	179	183		137	207	4 192	196	4 260		171			163	6 163 1
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peptidylprolyl iso	peptidylprolyl iso	peptidylprolyl iso	1	, †	Ran-binding protei	peptidylprolyl iso		CVCIONITION (CVD)	peptidylprolyl iso		ŕ	malic actd transpo	malic acid transpo	
CSHYAC	CSRTA	CSHUA	S66681	G82517	S58884	T07950	T06073	E84597	T50772	T12096	F84808	B64395	H64371	H82255
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164	164	165	301	113	3224	172	172	174	174	248	199	342	347	554
60.6	9.09	9.09	9.09	59.2	59.2	57.7	57.7	57.7	57.7	57.7	56.3	56.3	56.3	56.3
4 8 8	43	43	43	42	42	41	41	41	41	4.1	40	40	40	40
30 31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

) E
	isomerase
•	lylprolyl

peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat
NyAlternate names: cyclophilin B: PPIASE
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: S71547
R;Ruecknagel, K.P.; Pfeifer, T.; Rahfeld, J.U.; Schaerfke, M.; Fischer, G. submitted to the Protein Sequence Database, November 1996
A;Reference number: S71547
A;Accession: S71547

A.Molecule type: protein
A.Residues: 1-183 <RUE>
A.S.Residues: 10-183 <RUE>
A.S.Reperimental source: liver
C.S.Reperimental source: liver
C.S.Reywords: cis-trans-isomerase
F.1-183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental <MAT>
F.1-10-172/Domain: cyclophilin homology <CYP>

Gaps 100.0%; Score 71; DB 2; Length 183; 100.0%; Pred. No. 7:9e-05; ive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 11; Conservative

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1 NFKLKHYGPGW 11 ò q

7 RESULT

peptidylprolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999 C;Accession: A40516 F; Schneider, C. J. Biol. Chem. 266, 10739-10742, 1991 E.; Schneider, C. J. Biol. Chem. 266, 10739-10742, 1991 A;Title: S-cyclophilin. New member of the cyclophilin family associated with the secr A;Reference number: A40516; MUID:91250364 A;Reference number: A40516

A.Molecule type: mRNA A.Residues: 1-207 <CAR> A.Residues: 1-207 <CAR> A.Cross-references: GB-M63553; NID:g212648; PIDN:AAA49064.1; PID:g212649 C.Superfamily: peptidylprolyl isomerase; cyclophilin homology C.Keywords: cis-trans-isomerase; cyclosporin A binding F:34-196/Domain: cyclophilin homology <CYP>

Gaps ö Ouery Match

100.0%; Score 71; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels

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A:Status: preliminary
A:Nolecule types: mRNA
A:Roldcue; bypes: mRNA
A:Roldcue; bypes: mRNA
A:Roldcue; gypes: 
pertidylprolyl isomerase (EC 5.2.1.8) CyP-S1 precursor - mouse
N;Alternate names: cyclophilin B; cyclophilin-S1; cyclosporin A-binding protein
C;Species: Mus musculus (house mouse)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Jul-1999
C;Accession: A56861; B39722; S21835
R;Schumacher, A.; Schroter, H.; Multhaup, G.; Nordheim, A.
Biochim. Biophys. Acta 1129, 13-22, 1991
A;Title: Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a putative s A;Accession: A56861:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: teratocarcinoma F9 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:73234, NCBIP:73239)
A;Note: parts of this sequence, including the amino end of the mature protein, were R;Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
A;Note: parts of this 348-3491, 1991
A;Title: An endoplasmic reticulum-specific cyclophilin.
A;Reference number: A39722; MUID:91260697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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A; Description: The sequence of C. elegans cosmid F42G9.
A; Reference number: 218498
A; Accession: T16351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 71; DB 2; 1 100.0%; Pred. No. 9.3e-05;
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A;Molecule type: DNA
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A;Reference number: S21835
A;Accession: S21835
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A Molecule type: mRNA
A; Residues: 9-216 <HAS>
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A;Molecule type: mRNA
A;Residues: 1-216 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                    peptidylprolyl isomerase (EC 5.2.1.8) B precursor [validated] - human N.Alternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin C; Species: Homo sapiens (man) C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Dec-2000 C; Caccession: A39118; A39722; A40515; S65742 R; Proc. Rat., Zydowsky, L.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T. R; Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991 Aritle: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl isomer A; Reference number: A39118; MUID: 91156714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 'MLRLSERN',1-208 <SPI>
A; Residues: 'MLRLSERN',1-208 <SPI>
A; Cross-references: GB M63573, MDD:g337998; PIDN:AAA36601.1; PID:g337999
A; Cross-references: GB M63773, MDD:g337999; A; Note: the authors' translation begins at an ATG codon in poor context for intiation A; Note: the authors' translation begins at an ATG codon in poor context for intiation A; Note: parts of this sequence, including the amino end of the mature form, were confirm R; Mariller, C.; Allain, F; Kouach, M.; Spik, G.
Biochim. Blophys. Acta 1293, 31-38, 1996
A; Title: Evidence that human milk isolated cyclophilin B corresponds to a truncated form A; Reference number: S65742; MUID:96186273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence C;Comment: This protein binds to and is inhibited by the immunosuppressive drug cyclospe C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:g181250
M.; Maes, P.; Tartar, A.;
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A; Residues: 1-208 <PRI>
A; Cross-references: GB:M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335
R; Hasel, K. M.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
Mol. Cell. Biol. 11, 3484-4391, 1991
A; Title: An endoplasmic reticulum specific cyclophilin.
A; Reference number: A39722; MUID:91260697
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A; Residues: 1-208 < HAS>
A; Cross-references: GB-M60457; NID:g181249; PIDN:AAA35733.1;
A; Spik, G.; Haendler, B.; Delmas, O.; Mariller, C.; Chamoux,
J. Biol. Chem. 266, 10735-10738, 1991
A; Title: A novel secreted cyclophilin-like protein (SCYLP).
A; Reference number: A40515; MUID:91250363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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A, Molecule type: protein
A, Residues: 26-30;203 <MAR>
A, Experimental source: milk
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Best Local Similarity
Matches 11; Conserv
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peptidy|prolyl isomerase (EC 5.2.1.8) C precursor - human peptidy|prolyl isomerase (EC 5.2.1.8) C precursor - human c) Alternate names: cyclophilin C c; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Accession: 184204 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999 C; Accession: 184204 #; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurini, M.G.; Quesn Biochemiatry 33, 8218-88244, 1994 A; Title: Human cyclophilin C; primary structure, tissue distribution, and determinating A; Reference number: A54204; MuID:94304830 A; Accession: A54204 Aurol:94304830 A; Accession: A54204 Average A; Av
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Experimental source: kidney
A:Note: sequence extracted from NCBI backbone (NCBIN:149387, NCBIP:149388)
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                                        85.9%; Score 61; DB 2;
90.9%; Pred. No. 0.0046;
iive 0; Mismatches 1
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90.9%;
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Best Local Similarity
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 10; Conserv
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A;Gene: ROC7
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A54204
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Cell 66, 799-806, 1991
A;Title: Two cytoplasmic candidates for immunophilin action are revealed by affinity for
A;Reference number: A40047; MUID:91347379
A;Accession: A40047
A; Residues: 1-201 <TAI>
A; Cross-references: EMEL:U00051; NID:g1216305; PID:g485120; PIDN:AAA91355.1; CESP:F42G9.
A; Cross-references: EMEL:U00051; NID:g1216305; PID:g485120; PIDN:AAA91355.1; CESP:F42G9.
C; Genetics:
C; Genetics:
A; Gene: CESP: Cyp-6
A; Map position: 3
A; Introns: 66/3
A; Introns: 66/3
C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
C; Superfamily: peptidylprolyl isomerase
C; Superfamily: peptidylprolyl isomerase
F; 25-187/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptidylprolyl isomerase (EC 5.2.1.8) F31C3.1 [similarity] - Caenorhabditis elegans
N;Contains: cyclophilin
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A;Reference number: 219446
A;Accession: T21587
A;Accession: T21587
A;Accession: T21587
A;Molecule type: DNA
A;Residues: 1-204 <WILL.
A;Cross-references: EMBL: 292784; PIDN: CAB07192.1; GSPDB: GN00019; CESP:F31C3.1
A;Experimental source: clone F31C3
C;Genetics:
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun_1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.Contains: Cyclophilin
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C;Accession: T21587
C;Accession: T21587
S;Cottage, A.
submitted to the EMBL Data Library, March 1997
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A; Residues: 1-212 cRTS>
A; Residues: 1-212 cRTS>
A; Cross-references: GB:W74227; NID:g192898; PIDN:AAA37511.1; PID:g192899
C; Comment: This protein binds the immunosuppressive drug cyclosporin A.
C; Superfamily: peptidylproly1 isomerase: cyclophilin homology
C; Keywords: cis-trans-isomerase; cyclosporin A binding
F;37-199/Domain: cyclophilin homology <CXP>
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A;Introns: 69/3
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Reywords: cis-trans-isomerase
F;28-190/Domain: cyclophilin homology <CYP>
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 67; DB 2; Pred. No. 0.00042;
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Best Local Similarity 90.9
Matches 10; Conservative
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Matches 10; Conserv
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R.Jackson, K.; Soll, D. Mol. Genet. 262, 830-8, 1899
Mol. Gen. Genet. 262, 830-8, 1899
A;Title: Mutations in a new Arabidopsis cyclophilin disrupt its interaction with prot A;Title: Mutations in a new Arabidopsis cyclophilin disrupt its interaction with prot A;Teference number: 225117; MuID:20092489
A;Accession: T50838
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A;Experimental source: cultivar Wassilewskija
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptidylprolyl isomerase (EC 5.2.1.8) ROC7 [similarity] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: cyclophilin
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 24-Oct-2000
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                                                                                                                                                                                                                                                        Score 61; DB 2; Length 212
Pred. No. 0.0046;
0; Mismatches 1; Indels
A;Cross-references: GDB:136196; OMIM:123842
A;Cross-references: GDB:136196; OMIM:123842
A;Map position: 15q21-15q22
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Reywords: cis-trans-isomerase; cyclosporin A binding
F;37-199/Domain: cyclophilin homology <CYP>
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A;Molecule type: mRNA
A;Residues: 1-204 <JAC>
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A; Accession: T49204

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Patrickal Prolyl isomerase (EC 5.2.1.8) ROCZ - Arabidopsis thaliana N.Alternate names: cytosolic cyclophiln; peptidyl-prolyl cis-trans isomerase; protei C.Seciese Arabidopsis thaliana (mouse-ear cress) (Seciese Arabidopsis thaliana (mouse-ear cress) (C.Seciese) Arabidopsis thaliana (mouse-ear cress) (C.Seciese) (C.Se
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: 21-001-2000 #sequence_revision 21-Jul-2000 #text_change 24-Oct-2000
C.Sacession: T50837
R.Saito, T.; Niwa, Y.; Ashida, H.; Tanaka, K.; Kawamukai, M.; Matsuda, H.; Nakagawa,
Plant Cell Physiol. 40, 77-87, 1999
A.Title: Expression of a gene for cyclophilin which contains an amino-terminal endopl
A.Reference number: 225256; MUID:99205703
A.Secession: T50837
A.Secession: T50837
A.Secession: T50837
A.Secession: A.Secession: A.Secession of a gene for CB/EMBL/DDBJ
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A; Residues: 1-171,'N', 173-176 <CHO>
A; Cross-references: EMBL:U40400; NID:g1305456; PIDN:AAB96833.1; PID:g1305457
G; Genetics:
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A:Note: FLBO21:30
C:Superfamily: peptidylprolyl isomerase: cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding
F:3-171/Domain: cyclophilin homology cCVP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 201;
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A. Cross references: EMBL: AF020433; PIDN: AAB71401.1
A. Cross references: EMBL: AF020433; PIDN: AAB71401.1
A. Experimental source: Landsberg erecta
C. Genetics: CYP5
A. Genetics: CYP5
A. Genetics: CYP5
C. Superfamily: Peptidy prolyl isomerase; cyclophilin homology
C. Keywords: cis-trans-isomerase
F: 31-199/Domain: cyclophilin homology <CYP>
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Pred. No. 0.2;
0; Mismatches
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                   peptidylprolyl isomerase (EC 5.2.1.8) F27K19.100 (similarity] - Arabidopsis thaliana N;Alternate names: cyclophilin-like protein; protein F27K19.100
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 24-Oct-2000
C;Accession: T49204
R;Benes, V; Wurmbach, E; Drzonek, H; Ansorge, W; Mewes, H.W.; Rudd, S; Lemcke, K; Submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptidylprolyl isomerase (EC 5.2.1.8) ATCYP4 [similarity] - Arabidopsis thaliana N.Alternate names: cyclophilin C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: 21-Jul-2000 #sequence_revision 21-Jul-2000 #sequence_revision 21-Jul-2000
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R;Saito, T.; Ashida, H.; Kawamukai, M.; Matsuda, H.; Nakagawa, T.
R;Saito, T.; Ashida, H.; Kawamukai, M.; Matsuda, H.; Nakagawa, T.
Submitted to the EMBL Data Library, July 1995
A;Reference number: 225226
A;Accession: T50767
A;Status: prealiminary; translated from GB/EMBL/DDBJ
A;Residues: 1-176 <SAI>
A;Residues: 1-176 <SAI>
A;Experimental source: EMBL:U31370; PIDN:AAA74096.1
A;Experimental source: strain Landsberg
C;Gene: ATCYP4
C;Superfamily: peptidylprolyl isomerase; cyclophillin homology
C;Keywords: cis-trans-isomerase
C;Keywords: cis-trans-isomerase
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A:Molecule type: DNA
A:Residues: 1-234 <BEN>
A:Cross-references: EMBL:AL163832; GSPDB:GN00061; ATSP:F27K19.100
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A.Introns: 27/3; 49/3; 73/1; 89/1; 164/1; 189/2
C.Superfamily: peptidylprolyl isomerase; cyclophilin homology
C.Keywords: cistrans-isomerase
F:58-232/Domain: cyclophilin homology <CYP>
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DB 2; 0.17;

73.2%; Score 52; DB 81.8%; Pred. No. 0.17 tive 1; Mismatches

Conservative

q ò

Query Match Best Local Similarity Local 9; Conserva

71.8%; Score 51; DB 2; 90.0%; Pred. No. 0.2; 1ve 0; Mismatches

Conservative

Local Similarity les 9; Conserv 1 NFKLKHYGPG 10

Query Match Best Local Si Matches 9;

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Search completed: January 15, 2002, 13:06:16 Job time: 227 sec
1 NFKLKHYGPG 10
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Peptidylprolyl isomerase (EC 5.2.1.8) F23F1.12 - Arabidopsis thaliana peptidylprolyl isomerase (EC 5.2.1.8) F23F1.12 - Arabidopsis thaliana (mouse-ear cress)

C. Species: Arabidopsis thaliana (mouse-ear cress)

C. Species: Arabidopsis thaliana (mouse-ear cress)

C. Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001

C. Accession: T02489; G84702

R. Rounsiey, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaull R. Rounsied to the EMBL Data Library, August 1998

A. Becreated number: 214675

A. Reference number: 214675

A. Reference number: 214675

A. References: EMBL-AC004680; NID:93420043; PIDN:AAC31856.1; PID:93420055

A. Cross-references: EMBL-AC004680; NID:20083487

A. Reference number: A84420; MUID:20083487

A. Reference number: A84420; MUID:20083487

A. Starlus: Arabidopsis thalianary
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C; Species: Trichoderma harzianum
C; Species: Trichoderma harzianum
C; Species: Trichoderma harzianum
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: 333212
R; Vasseur, V.V.; van Montagu, M.M.; Goldman, G.G.H.
R; Vasseur, V.V.; van Montagu, M.M.; Goldman, G.G.H.
A; Description: Molecular Library, April 1993
A; Rescription: Molecular characterization of mycoparasitic-related genes of Trichoderma A; Reference number: S33212
A; Accession: S33212
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A;Molecule type: DNA
A;Residues: 1-201 <STO>
A;Residues: 1-201 <STO>
A;Cross-references: GB:AE002093; NID:g3420055; PIDN:AAC31856.1; GSPDB:GN00139
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A;Status: DNA
A;Residues: 1-573 «VAS>
A;Residues: 1-573 «VAS>
A;Cross=references: EMBL:222594; NID:9296569; PIDN:CAA80308.1; PID:9296570
C;Superfamily: arginine permease
C;Superfamily: arginine permease
C;Keywords: amino acid transport; glycoprotein; transmembrane protein
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Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels
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A;Introns: 22/3; 46/1; 62/1; 70/1; 131/1
A;Note: F23F1.12
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Superfamily: peptidylprolyl isomerase; cyclosporin A binding E;31-199/Domain: cyclophilin homology <CYP>
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                                       122 NFKLKHTGPG 131
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us-09-720-469-5.rpr

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein · protein search, using sw model

January 15, 2002, 13:14:59; Search time 24.88 Seconds (Without alignments) 16.210 Million cell updates/sec Run on:

US-09-720-469-5 71 1 NFKLKHYGPGW 11 Title: Perfect score: Sequence: 100059 seqs, 36664827 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ptio	P24367 aallus aall	bos tas		mus I			~	_	_	P34054 trichoderma	P52018 caenorhabdi	P54985 blattella q	rattus nor	P30405 homo sapien		P34791 arabidopsis		P52015 caenorhabdi	P52011 caenorhabdi	_	P14851 cricetulus	P17742 mus musculu		P05092 homo sapien	mus m	Q9unp9 homo sapien	bos		arabi	ol vicia faba	72		~
SUMMARIES		ΩI	Ω,	CYPB_BOVIN	CYPB_HUMAN	CYPB_MOUSE	CYPB_RAT	CYP6_CAEEL	CYP5_CAEEL	CYPC_HUMAN	CYPC_MOUSE	INA1_TRIHA	CYPB_CAEEL	CYPH_BLAGE	CYPM_RAT	CYPM_HUMAN	CYP1_CAEEL	CYP4_ARATH	CYP2_CAEEL	CYP7_CAEEL	CYP3_CAEEL	CYPH_BOVIN	CYPH_CRILO	CYPH_MOUSE	CYPH_RAT	CYPH_HUMAN	CYPE_MOUSE	CYPE_HUMAN	RBP2_BOVIN	RBP2_HUMAN	CYP1_ARATH	CYPB_VICFA	Y762_METJA	Y576_METJA	ASNS_SANAU
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		Match Length	207	208	208	208	208	201	204	212	212	573	183	164	206	207	192	260	171	171	173	163	163	163	163	164	298	301	1085	3224	172	248	342	347	524
æ	Query	Match	ö			100.0	100.0	94.4	88.7	85.9	85.9	0.69	9.79	66.2	64.8	64.8	63.4	63.4	62.0	62.0	62.0	9.09	9.09	90.0	90.0	60.6	60.6	9.09	59.5	59.5	57.7	57.7	56.3	56.3	56.3
		Score	71	71	71	71	71	29	63	61	61	4 .	44. 30 i	4	46	40	45	45	44	44	44	43	Δ. ω	4.	4.	4. A. (4.						40		40
	Result	No.		7	m	*	S	91	7	a o (on (10	11	77	13	14	15	16	17	18	61	20	21	77	23	47	57	97	/7	28	53	30	31	32	33

P49092 lotus Japon	P19251 Disum sativ	P49093 10tus Janon	O24661 triphysaria	P31752 asparadus o	09u3v9 drosophila	P25007 drosophila	P19252 pisum sativ	P57923 pasteurella	P43827 haemonhilus	P23615 saccharomyc	P24525 brassica na
ASN1_LOTJA	ASN1 PEA	ASN2 LOTTA	ASNS TRIVS	ASNS_ASPOF	XMS2_DROME	CYPH_DROME	ASN2_PEA	SYL PASMU	SYL_HAEIN	SPT6 YEAST	CYPH_BRANA
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585	585	585	585	589	1184	165	582	860	861	1451	171
56.3	56.3	56.3	56.3	56.3	56.3	54.9	54.9	54.9	54.9	54.9	53.5
0	40	40	40	40	40	33	39	39	39	39	38
4											

ALIGNMENTS

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Gaps

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Query Match 100.0%; Score 71; DB 1; Length 207; Best Local Similarity 100.0%; Pred. No. 3.6e-05; Matches 11; Conservative 0; Mismatches 0; Indels

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Best Local Similarity
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CYPB_HUMAN
                               Matches
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                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bose S., Muecke M., Freedman R.B.;
The characterization of a cyclophilin-type peptidyl prolyl
cis-transisomerase from the endoplasmic-reticulum lumen.";
Biochem. J. 300:871-875(1994).
Elochem. J. 300:871-875(1994).
-I-FUNCTION: PPTASES ACCELERATE THE FOLDING OF PROTEINS.
-I-CATALYTICA. PATASES ACCELERATE THE FOLDING OF PROLINE IMDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
-I-BAZNAR REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
-I-SUNCELLULAR LOCATION: BUDOPLASMIC RETICULUM LUMEN.
-I-SUMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carrello A., Mark P.J., House A.K., Ratajczak T.;
Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREVENT SECRETION FROM ER
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0097C88289AF6276 CRC64;
                                                                                                                                                                                                                                              208 AA
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InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRNTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                              PRT;
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MEDLINE-94280416; Pubmed-8010972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94283623; PubMed-8013656;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to cyclophilin-A.";
FEBS Lett. 347:31-36(1994).
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208
                                                                 118 NFKLKHYGPGW 128
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199
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208 AA;
                                  1 NFKLKHYGPGW 11
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P80311;
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ID CYPB_BO

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DB 1; Length 208;

Score 71;

100.08;

Query Match

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MEDINE-22112948; PubMed-1530944;
Arber S., Krause K.-H., Caronl P.;
"S-cyclophilin is retained intracellularly via a unique COOH-terminal
sequence and colocalizes with the calcium storage protein
calreticulin.";
                                                                                                                                                                       CYPB_HUMAN STANDARD; PRT; 208 AA.
P23284;
01-NOV-1991 (Rel. 20, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMBRASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
PROTABANSE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
PPIB OR CYPB.
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94255495; PubMed-8197205; Mikol V., Kallen J., Walkinshaw M.D.; "X-ray structure of a cyclophilin B/cyclosporin complex: comparison with cyclophilin A and delineation of its calcineurin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes."; Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl isomerase with a signal sequence.";
Proc. Natl. Acad. Sci. U.S.A. 88:1903-1907(1991).
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                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDIATE-91250363; PubMed-2040592;
MEDIATE-91250363; PubMed-2040592;
Spik G., Haendler B., Delmas O., Mariller C., Chamoux M., Mae Tartar A., Montreuil J., Stedman K., Kocher H.P., Keller R., Hiestand P.C., Movva N.R.;
An novel secreted cyclophilin-like protein (SCYLP).";
J. Biol. Chem. 266:10735-10738(1991).
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 26-40.
MEDLINE-91156714; PubMed-2000394;
Price E.R., Zydowsky L.D., Jin M., Hunter C.H., McKeon F.D., Walsh C.T.;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 2-208 FROM N.A.
MEDLINE-91260697; PubMed-1710767;
MEDLINE-1700697; PubMed-1710767;
Manacl K.W., Glass J.R., Godbout M., Sutcliffe J.G.
"An endoplasmic reticulum-specific cyclophilin.";
Mol. Cell. Biol. 11:3484-3491(1991).
          Pred. No. 3.6e-05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
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MEDLINE-93162043; PubMed-1286667;
100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Cell Biol. 116:113-125(1992).
                             Conservative
                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION.
                                                                                   119 NFKLKHYGPGW 129
                                                             1 NFKLKHYGPGW 11
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SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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Matches 11; Conserv
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P24368;
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            SPETT MEN WENT AND DESCRIPTION OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1999 (Rel. 38, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-SI).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISKRASE.
PROSTTE; PS00170; CSA_PPIASE_1; 1.
PROSTTE; PS500772; CSA_PPIASE_2; 1.
Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family; 3D-structure.
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  -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 208;
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SEQUENCE FROM N.A.
MEDLINE-91260697; PubMed-1710767;
Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.,
"An endoplasmic reticulum-specific cyclophilin.";
Mol. Cell. Biol. 11:3484-3491(1991).
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                                                                                                                                                                                                             M63573; AAA36601.1; ALT_INIT.
M60457; AAA35733.1; -.
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                                                                                                                                                                                         EMBL; M60857; AAA52150.1; -.
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Best Local Similarity 100.
Matches 11; Conservative
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208
208
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PIR; A40515; A40515.
PDB; 1CYN; 29-JAN-96.
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SEQUENCE FROM N.A.
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J. Cell Biol. 116:113-125(1992).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
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01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B RRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-SI).
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Arber S., Krause K.-H., Caroni P.;
"S-cyclophilin is retained intracellularly via a unique COOH-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
PREVENT SECRETION FROM ER
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Iwai N., Inagami T.;
"Molecular cloning of a complementary DNA to rat cyclophilin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam: PF00160; pro_isomerase: 1.
PRINTS: PR00153; CSAPISMASE.
PROSITE: P800170; CSA_PPTASE_1: 1.
PROSITE: P550072; CSA_PPTASE_2: 1.
Cyclosporin: Isomerase: Rotamase: Signal; Endoplasmic reticulum; Multigene family: 25 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 71; DB 1; Length 208; 100.0%; Pred. No. 3.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence and colocalizes with the calcium storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY),
4B8DF5AE40BAD3A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                             EMBL; M60456; AAA37498.1; -. EBBL; X58990; CAA41736.1; -. PIR; B34727. P3777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:97750; Ppib.
InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kidney Int. 37:1460-1465(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22713 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
208
208
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PIR; S21835; S21835.
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CYP5_CAEEL P52013;
                                                    CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                    Query Match
                                                                                                                                                                                                             RESULT 7
CYP5_CAEEL
                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1997 (Rel. 35, Last annotation update)
PEPTIDKL-PROLYL CIS-TRANS ISOMERASE 6 PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN-6).
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-96276416; PubMed-8694762;
Page A.P., Macniven K., Hengartner M.O.;
Page A.P., Macniven Contracterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegans.";
Biochem. J. 317:179-185(1996).
                                                                                                                          Β.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                           ISOMERASE
HSSP; P23284; ICYN.
HSSP; PSO01010; CSA_PPISASE.
HSOSTE; PSO01010; CSA_PPISASE.
HSSSTE; PSO0102; CSA_PPIASE.1; I.
HSSSTE; PSSO017: ISOMERASE, ROLAMASE, SIGNAL; Endoplasmic reticulum; Wultigene family.
                                                                                                                                                                                                                         ö
                                                                                                                                                                                               Length 208;
                                                                                                                                                                                                                        Indels
                                                                                                               BY SIMILARITY.
PEPTIDYL-PROLYL CIS-TRANS
PREVENT SECRETION FROM ER
(BY SIMILARITY).
                                                                                                                                                             76D12AC3427FEF32 CRC64;
                                                                                                                                                                                                Score 71; DB 1; L
Pred. No. 3.6e-05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                 201 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WormPep, F42G9.2; CE01301.
InterPro: IPR002130; CSA_PPIase.
Pfam: PP00160; pro_isomerase: 1.
PRINTS; PR00153; CSAPPISMRASE.
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                                                                                                                                                                                               100.0%;
ilarity 100.0%;
Conservative 0;
                                                                                                                                                              23025 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U00051; AAA91355.1;
                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                               208
208
208
                                                                                                                                                                                                                                                            119 NFKLKHYGPGW 129
                                                                                                                                                                                                                                                1 NFKLKHYGPGW 11
                                                                                                                                                                AA;
                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                CYP6_CAEEL
P52014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taich A.;
                                                                                                                                                              SEQUENCE
                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                      CYP6_CAEEL
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Last annotation update)
ANNS ISOMERASE 5 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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NCBI_TaxID=6239;
                                            POTENTIAL.
PEPTINYL-PROLYL CIS-THANS ISOMERASE 6.
N-LINKED (GLCARC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page A.P., Macniven K., Hengartner M.O.;
Cloning and blochemical characterization of the cyclophilin
homologues from the free-11ving nematode Caenorhabditis elegans.";
Blochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-i- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-i- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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                                                                                                                                                                                                   Length 201;
                                                                                                                                                                                                   Score 67; DB 1; Length 201
Pred. No. 0.00017;
L; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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SEQUENCE 204 AA; 22366 MW; 22ABB39AD1127BAA CRC64;
                                                                                                       084C5762917F958B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50072; CSA_PPIASE_2; 1.
ISOMERASE; Rotamase; Multigene family; Signal.
SIGNAL 16 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Pfam: PF00160; pro_isomerase; 1.
PROSITE: PR00153; CSAPPIARASE.
PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-96276416; Pubmed-8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seq
01-NOV-1997 (Rel. 35, Last ann
PEPTIDYL-PROLYL CIS-TRANS ISOM
                                                       1 16 P
17 201 P
130 130 N
201 AA; 21864 MW;
                                                                                                                                                                                                      94.4%;
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                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 NFKLKHYGAGW 122
                                                                                                                                                                                                                                                                                                                                          109 NFKLQHYGPGW 119
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                                                                                                                                                                                                                                                                                                       1 NFKLKHYGPGW 11
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Matches 10; Conserv
                                                                                                                                                                                                                             Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CYCLOPHILIN-5).
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HSSP, P05092; ZRMC.
MGD; MGI:97751; Ppic.
InterPro; IPR002130; CSA_PPIase.
Pfan, PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
MEDLINE-91347379; PubMed-1652374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.98;
                                                                                                                                                                                                                                                                                                                                                              EMBL; M74227; AAA37511.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rrichoderma harzianum.
                                                                                                                                                                                                                                                                                                                                                                                  ; A40047.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyclosporin;
SEQUENCE 2
                                                                                                                                                                                                                                                                                                                                                                                A40047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INA1_TRIHA P34054;
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                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYPC_MOUSE STANDARD; PRT; 212 AA. p30412; p10412; class rel 25, Created) class rel 25, Last sequence update) class (Rel. 25, Last sequence update) class (Rel. 32, Last annotation update) PEPTIOYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAWASE) (CYCLOPHILIN C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                               MEDLINE-94304830; PubMed-8031755; Schmitz R., Wehrli S., Mikol V., Schmeider H., Charara N., Schmitz R., Wehrli S., Mikol V., Zurini M.G., Quesniaux V.F., Movva N.R.; Human cyclophilin C: primary structure, tissue distribution, and determination of binding specificity for cyclosporins."; Biochemistry 33:8218-8224(1994).

1. FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

1. CATALYTIC ACTIVITY: CIESTRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLGOPEPTIDES.

1. ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.

1. SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.9%; Score 61; DB 1; Length 212; 90.9%; Pred. No. 0.0019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyclosporin; Isomerase; Rotamase; Multigene family.
SEQUENCE 212 AA; 22763 MW; 6F3DB547A2AE581B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam: PF00160; Pro_isomerase; 1.
PRINTS; PR00153; CSAPPISRRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002130; CSA_PPlase.
                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S71018; AAB31350.1; -.
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Matches 10; Conservative
          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                 Homo sapiens (Human).
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                               PPIC OR CYPC
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MIM; 123842;
       CYPC_HUMAN P45877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
CYPC_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Friedman J., Weissman I.L.;
Two cytoplasmic candidates for immunophilin action are revealed by
affinity for a new cyclophilin; one in the presence and one in the
absence of CsA.";
                                                                                                                     STRAIN-IMI 206040;
MEDLINE=95291429; PubMed=7773384;
Vasseur V.V., van Montagu M.M., Goldman G.G.H.;
"Trichoderma harzianum genes induced during growth on Rhizoctonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Trichoderma.
NCBI_TaxID=5544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Isomerase, Rotamase, Multigene family.
212 AA; 22794 MW; C99E7AA5D0FA04B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microbiology 141:767-774(1995).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- INDUCTION: DURING MYCOPARASITISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61; ____
Pred. No. 0.0019;
__trhes 1;
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01-FEB-1994 (Rel. 28, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
AMINO-ACID PERMEASE INDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      573 AA
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EMBL; Z66499; CAA91297.1;
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                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P05092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyclosporin;
SEQUENCE 1
                                                                                                                                                                                                                                               CYPH_BLAGE
P54985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                     CYPH_BLAGE
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                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page A.P., Macniven K., Hengartner M.O.;
*Cloning and blochemical characterization of the cyclophilin
homologues from the free-living nematode Caenorhabditis elegans.";
Blochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PIPASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                              01-0cT-1996 (Rel. 34, Last Sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 11 (EC 5.2.1.8) (PPIASE)
(FOTAMANS) (CYCLOPHILIN-11).
                                                                                                                                                                                                                                              Score 49; DB 1; Length 573;
Pred. No. 0.55;
1; Mismatches 1; Indels
                                                                                                                                                                                                                5FB0A806934DB55D CRC64;
                                                                                  transport; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                  183 AA.
                                       InterPro; IPR002293; AA_rel_permease_1.
InterPro; IPR002027; AMIno_acid_permease.
Pfam; PF00324; aa_permeases; 1
PROSITE: PS00218; AMINO_ACID_PERMEASE_1; 1.
or send an email to license@isb-sib.ch).
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MEDLINE-96276416; Pubmed-8694762;
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80.0%;
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                    EMBL; Z22594; CAA80308.1;
                                                                                                                                                                                                                 62850
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         CYP-11 OR T01B7.4.
Caenorhabditis elegans.
                                                                                                        1117
2200
229
229
280
315
371
                                                                                   Transport; Amino-acid
                                                                                                                                                                                                                573 AA;
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                         1 NFKLKHYGPG 10
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                CYPB_CAEEL
P52018;
                                                                                                                                                                                           TRANSMEM
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                             RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Trachéata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattarla;
Blaberoidea; Blattellidae; Blattellinae; Blattella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 164;
                                                                                                                                                                                                                                       Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 AA; 17935 MW; ASE25B574DFCDC99 CRC64;
                                                                                                                                               Isomerase; Rotamase; Multigene family.
SEQUENCE 183 AA; 20193 MW; 23549C922828C533 CRC64;
                                                                                                                                                                                                                                                                                       ;;
                                                                                                                                                                                                                                          DB 1;
0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 1;
Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 AA
                                                                                                                                                                                                                                          Score 48; DB Pred. No. 0.27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blattella germanica (German cockroach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
MOST, FOURT 4; CE03588.
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PROSITE; PR00153; CSAPPISMASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.2%;
80.0%;
                                                                                                                                                                                                                                          67.6%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X87418; CAA60869.1; -.
                                                                                                                                                                                                                                       Query Match 67.6
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                               ||:||| |||
105 NFELKHIGPG 114
                                                                                                                                                                                                                                                                                                                                1 NFKLKHYGPG 10
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Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92078192; PubMed-1744118;
MEDLINE-92078192; PubMed-1744118;
MEDLINE-92078192; PubMed-1744118;
MEDLINE-92078192; PubMed-1744118;
Mergama D.J., Eder C., Gross M., Kersten H., Sylvester D.,
Appelbaum E., Cusimano D., Livi G.P., McLauglin M.M., Kasyan K.,
Appelbaum E., Cusimano D., Livi G.P., Mand A., Prichett W.P.,
Aporter T.G., Silverman C., Dunnington D., Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Dunnington D., Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Dunnington D., Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Dunnington D., Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Dunnington D., Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Dunnington D., Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Dunnington D., Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Corp. Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Corp. Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Corp. Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Corp. Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Gross A., Prichett W.P.,
Aporter T.G., Silverman C., Gross France T.G., Sunction T.G., Sunction C., Corp. Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Gross T.G., Gross T.G., Sunction C., Corp. Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Gross T.G., Silverman C., Gross T.G., Silverman C., Gross T.G., Silverman C., Gross T.G., Corp. Hand A., Prichett W.P.,
Aporter T.G., Silverman C., Gross T.G., Silverman 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclosporin; Isomerase; Rotamase; Multigene family; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDYE-PROLYL CIS-TRANS ISOMERASE.
D7C76F1D4049F16A CRC64;
                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Last Sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PPROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR
(EC 5.2.1.8) (PPIASE) (ROTAWASE) (CYCLOPHILIN F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITOCHONÚRION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 1;
Pred. No. 0.67;
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(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                           207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro: IPR00130; CSA_PPIBASE.
Pfam: PP00160; pro_isomerase: 1.
PROSITE: PR00153; CSAPPIBARASE.
PROSITE: PS00170; CSA_PPIBASE_1: 1.
PROSITE: PS50072; CSA_PPIBASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 207 PE
207 AA; 22040 MW;
                                                                                                                                                                                 25, Created)
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M80254; AAA58434.1; -.
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                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A41581; A41581.
HSSP; P05092; 3CYS.
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128 NFTLKHVGPG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606
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01-OCT-1996
20-AUG-2001
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P52009;
                                                                                                                              CYPM HUMAN
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SEQUENCE
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                                                                                                CYPM_HUMAN
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"Purification and N-terminal sequencing of peptidyl-prolyl cis-trans-
isomerase from rat liver mitochondrial matrix reveals the existence
of a distinct mitochondrial cyclophilin.";
Biochem. J. 284:381-385(1992)
--- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
--- FUNCTION: OIS-TRANS ISOMERIZATION OF PROLINE IMDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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PRIMES, PRO015; CSAPPISMRASE.
PROSTIE: PSS00170; CSA_PPIASE_1; 1.
PROSTIE: PSS0072; CSA_PPIASE_2; 1.
Cyclosporin; Isomerase; Rotamase; Multigene family; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
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SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR (EC_5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-WISTAR; TISSUE-Skeletal muscle;
Price N.T., Woodfield K.Y., Halestrap A.P.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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69048482631B9FAD CRC64;
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Mismatches
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InterPro; IPR002130; CSA_PPIase.
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Best Local Similarity
                                             1 NFKLKHYGPG 10
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87 NFQLKHTGPG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10116;
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PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
                  (CYCLOPHILIN-1).

CYP-1 OR Y49A3A.5.

Caenorhabditis elegans.

Elvaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                 Page A.P., Macniven K., Hengartner M.O.;
"Cloning and biochemical characterization of the cyclophilin
homologues from the free-living nematode Caenorhabditis elegans.";
Biochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                 -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isomerase; Rotamase; Multigene family.
SEQUENCE 192 AA; 20710 MW; C2094D91809ECE85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U30943; AAC47116.1; --
EMBL; AL033512; CAA22075.1; --
HSSP; P05092; 1AWV.
WOFENPER; Y49A3A.5; CE22213.
InterPro; IPR002130; CSA_PPIASE.
PRINTS; PR00160; pro_isomerase; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-96276416; Pubmed-8694762;
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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Search completed: January 15, 2002, 13:14:59 Job time: 655 sec

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2; Indels

63.4%; Score 45; DB 1; Length 192; 80.0%; Pred. No. 0.92; 1ive 0; Mismatches 2; Indels

Query Match
Best Local Similarity 80.0
Matches 8; Conservative

112 NFDLKHTGPG 121

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1 NFKLKHYGPG 10

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                                      O9fy98 arabidopsis
O9ass6 arabidopsis
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Q9zt54 griffithsia
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09uh01 homo sapien
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periplaneta
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                                                              O9nou4 macaca mula
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Kainer D.B., Doris P.A.;

The object of the control                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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100.0%; Score 71; DB 11; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN B (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                  208 AA
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O9bvK5 homo sapien
O9dvy1 mus musculu
O917v3 drosophila
O62190 caenorhabdi
O9w27 drosophila
O44073 tachypleus
Q27774 schistosoma
Q29p08 sus scrofa
O9sp02 arabidopsis
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038901 arabidopsis
091974 arabidopsis
021515 arabidopsis
080876 arabidopsis
040672 oryza sativ
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Q25093 hirudo medi
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  GenCore version
Copyright (c) 1993 - 2000
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                                             OM protein - protein search, using sw model
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Listing first 45 summaries
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KRAID. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakava T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Atawa T., Hara A., Ribata Y., Kolono H., Kaukawa T., Saito R.,

A Atawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Golobori T., Bono H., Kaukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Robin P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Tomita M., Wagner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonado M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonado M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Romostel M.J., Hull D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Radota R., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Radota R., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Radota R., Ruzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Radota R., Radota R., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Radota R., Radota R., Wang K.H., Weitz C., Whittaker C., Wilming L.,

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Radota R.,
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Functional annotation of a full-length mouse cDNA collection.";
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0
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-SKIN, AND MELANOMA;
Strausberg R.;
Submitted (DEC.2000) to the EMBL/GenBank/DDBJ databases.
EMBL; BC001125; AAH01125.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2D0410A07AA9E420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                    01-JUN-2001 (TremBLrel. 17, Last sequence update) 01-JUN-2001 (TremBLrel. 17, Last annotation update) PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 AA.
                                                                                                          216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002130; CSA_PPIase.
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EMBL; AKO02357; BAB22036.1; -.
MGD; MGI:97750; Pplb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 AA; 23742 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, PEPTIDYLPROLYL ISOMERASE B.
                                                                                                                                                            (TrEMBLrel. 17, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity luv...
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 NFKLKHYGPGW 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NFKLKHYGPGW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki Y.;
                                                                                                                                                                 01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                           Q9BVK5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09DCY1
                                                                                                                09BVK5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
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                                                            RESULT
Q9BVK5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9DCY1
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RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A. Adams M.D. Celniker S.E., Holt R.A., Evans R.A., Galle R.F., Ananatidas B.G., Scherer S.E., I.I. P.W., Hoskins R.A., Galle R.F., Gocayor R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Statchon G.G., Worthan J.R., Yandell M.D., Zhang Q., Chan L.X., F. Arandon R.G., Roders Y. H.C., Blazel R.G., Change M., Pietiffer B.D., R.A. Bardon R.G., Change M., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Nalomkoch C., Baldwin D., R.A. Besson K.Y., Benson P.V., Barsendale J., Bayterkaroglu L., Beasley E.M., Besson R.Y., Benson P.V., Barsendale J., Bayterkaroglu L., Beasley E.M., Besson K.Y., Benson P.A., Buttler H., Cadleu E., Center A., Chandra I., R. Bortsy J.M., Cawley S., Dahlke C., Davamport L.B., Davise P., Brattler P., R. Dobchen M.R., Bouds J., Brokstein P., Brottze P., R.A. Cherry J.M., Cawley S., Dahlke C., Davamport L.B., Davise P., Cherry J.M., Cawleu E., Center A., Chandra I., R.A. Dobelor B., Domes M., Dugan-Rocha S., Dunkov B.C., Dunn P., R.A. Dober J., E., Downes M., Dugan-Rocha S., Punkov B.C., Dunn P., R.A. Harris N.L., Evangelista C.C., Ferraz C., Ferraz C., Gabriellan A.E., Garg N.S., Galbart W.M., Glasser K., R. Albail M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A., Hostin D., Houston K.A., Howland T.J., Weil M.-H., Ibeywam C., Rabila M., Ralush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A. Merkulov G. Milshina N.V. Moharny C., Morris J., Moster B., McIntoon K.A., Mullan, W. Morles B., McIntoon K.A., Mullan, W. Morles B., McIntoon K.A., Mullan, C., Siden-Klamos I., Shangon M., Stupski M.P., Shan K., Man K., Mansen B.C., Siden-Klamos I., Shangon M., Stupski M.P., Shan K., Man K., Shue B.C., Scheeler F., Shan H., K., Ramington K., Rabinsoon M., Stupski M.P., Shu B., Shu B.C., Shan M., Welley B., Milliams S.M., Woodage T., Worley K.C., Wu Supski M.P., Shu B.C., Shang X.H., Woodage T., Shang M., Luu X., Massaman D.A., Walliams S.M., Woodage T., Worley K.C., Wu S., Shu B.C., Shang X.H., Wooda
                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Bphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                    Length 216;
                                                                                                                                                                                                                                                                                           Indels
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS50072; CSA_PPIASE_2; 1.
SEQUENCE 216 AA; 23713 MW; CE9DAD1544AE72FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                    Score 71; DB 11;
Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 AA.
                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20196006; PubMed-10731132;
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                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  127 NFKLKHYGPGW 137
                                                                                                                                                                                                                                                                                                                                                                     1 NFKLKHYGPGW 11
                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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InterPro; IPR002130; CSA_PPIase.

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CG2852
                                                                     09W227
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                                   RESULT
09W227
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Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

A dardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

A Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Lightning J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M.,

Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownkeen R.,

Raidon N., Smith A., Sonnhammer E., Staden R., Walston J.,

Thierry-Mieg J., Thomas K., Vaudin M., Waughan K., Waterston R.,

Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

The Equation M. PeptidyL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLDING OF PROTEINS (BY SIMILARITY).

-:- CATALYTICA CTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMDIC PEPTIDE BONDS IN OLIGOREPITIORS.

-:- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.

EMBL: Z92784; CABO7192.1;

HSSP; P23284; ICYN.

Interpro: PRO02130; CSA_PPISASE.

PFEMR: PF00160; pro_isomerase: 1.

PRINTS; PRO0153; CSAPPISMRASE.
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Pred. No. 0.0029;
0; Mismatches 1; Indels
                                                                                                                     88.7%; Score 63; DB 5; Length 120; 90.9%; Pred. No. 0.0016; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cottage A.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                   CF93898B694FA9F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21927 MW; 6216192BFE1FB493 CRC64;
                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYP-5 PROTEIN (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                         204 AA.
                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
             Pfam; PF00160; pro_isomerase: 1.
RNINTS; PR00153; CSAPPISMRASE.
PROSITE; PS50072; CSA_PPIASE_2: 1
SEQUENCE 120 AA: 12362 MW; CFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94150718; PubMed-7906398;
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90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 88.7
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                     Query Match 88.7
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
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                                                                                                                                                                                              1 NFKLKHYGPGW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 AA;
                                                                                                                                                                                                                   27 NFKLKHYGAGW 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                       062190
                                                                                                                                                                                                                                                                                    RESULT
062190
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REF STRAIN-BERKELER:
RA GADGENE FOLKE S.E. LIP.M., Hoskins R.A., Galle R.E.,
RAGENING S.C., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RAGAMS W.D., Cellniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RAGAMS W.D., Cellniker S.E., Holt R.A., Evans G., Chen L.X.,
Sutron G.G., Wortuman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutron G.G., Wortuman J.R., Yandell M.D., Zhang G., Feiffer B.D.,
RA Baradon R.C., Rogers Y.H.C., Blazel R.G., Chenner M., Henderson S.N.,
RA Baradon R.C., Rogers Y.H.C., Blazel R.G., Chenner M., Bindon G.R., Miklos G.L.G.,
Abril J.F., Agbayani A., Baxendale J., Bayraktarolyl L., Beasley E.M.,
RA Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Briskstein P., Brottler P., Brottler P.,
Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Buttis K.D., Ewnose P.V., Berman B.P., Bhandari D., Bolshakov S.,
Buttis K.D., Botchan M.R., Bouck J., Buyaktaroly B., Botskakov S.,
Buttis K.J., Evangeliste C.C., Ferrac C., Ferrac S., Dunkov B.C.,
Buttis K.J., Evangeliste C.C., Ferrac C., Ferrac S., Dunkov B.C.,
RA Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Harris N.L., Harvey D., Heiman T.J., Well M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Well M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Well M.-H., Ibegwam C.,
RA Harris N.L., Marvey D., Heiman T.J., Well M.-H., Ibegwam C.,
RA Harris N.L., Marvey D., Heiman T.J., Well M.-H., Ibegwam C.,
RA Harris N.L., Marvey D., Heiman T.J., Well M.-H., Ibegwam C.,
RA Harris N.L., Marvey D., Heiman T.J., Well M.-H., Ibegwam C.,
RA Harris N.L., Marvey D., Heiman T.J., Well M.-H., Ind. Z., Liang Y. Lin X.,
RA Harris N.L., Marvey D., Warph B., Murphy B., Murph
                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda: Tracheata; Hexapoda: Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

    -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
TRANS ISOMERASE FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOLDING OF PROTEINS (BY SIMILARITY).
                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P23284; ICYN.
FlyBase; FBgn0034753; CG2852.
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003458; AAF46873.1; -
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                   Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                       CG2852 PROTEIN.
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Gaps

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112 NFKLKHYGAGW 122

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1 NFKLKHYGPGW 11

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044073; 044073

RESULT 044073

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Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoldea; Schistosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-SMALL INTESTINE;
MEDLINE-95237607; bubmed-8672129;
MEDLINE-95237607; bubmed-8672129;
Minteroe A.K., Fredholm M., Davies W.;
Evaluation and characterization of a porcine small intestine cDNA library; analysis of 839 clones.";
Mamm. Genome 7:509-517(1996).
MARM. Genome 7:509-517(1996).
MEMBL: F14628; CAA21162.1; -.
HSSP; P23284; 1CYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metázoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
9551 MW; EB3EA68ED630AE97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 5;
Pred. No. 0.073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfan; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pram; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                 MEDLINE-97053959; PubMed-8898338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002130; CSA_PPlase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 AA; 23238 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U50389; AAC47316.1; -. HSSP; P23284; 1CYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.5%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.5
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYCLOPHILIN B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
213
213
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                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
                                                                            NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
                                                                                                                                                         STRAIN-CHINESE
                                                          Schistosoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
NON_TER
SEQUENCE
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
(ROJAMASE) (CYCLOPHILIN G) (P27).
Tachypleus tridentatus (Japanese horseshoe crab).
Elwaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura; Limulidae; Tachypleus.
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1999 (TrEMBLrel. 09, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIOYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE B) (ROTAMASE B) (CYCLOPHILIN B) (S-CYCLOPHILIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takaki Y., Muta T., Iwanaga S.;
"A peptidyl-prolyl cis/trans-isomerase (cyclophilin G) in regulated secretory granules.";
J. Biol. Chem. 272:28615-28621(1997).
-i- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. MAY PLAY FROLE IN MAINTAINING THE CONFORMATIONAL INTEGRITY OF STORED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPTIDYL-PROLYL CIS-TRANS ISOMERASE G. 728CB63EBB821C68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-:- ENZYME REGULATION: INHIBITED BY CYCLOSPORIN A (CSA).
-:- TISSUE SPECIFICITY: HEMOCYTE LARGE SECRETORY GRANULES.
-:- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPISSE_1; 1.
PROSITE; PS50072; CSA_PPISSE_2; 1.
CYCLOSPORIN; Isomerase; Rotamase; Signal; Multigene family.
                                                                            Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63; DB 5; Length 220;
Pred. No. 0.0031;
                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
22199 MW; A9CEF88B1CC813F7 CRC64;
                                                                       Score 63; DB 5;
Pred. No. 0.0029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 AA.
                                                                                                                                                                                                                                                                                                                                                        220 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-HEMOCYTE;
MEDLINE-98019238; Pubmed-9353327;
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InterPro; IPR002130; CSA_PPIase.
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90.9%;
                                                                       88.7%;
90.9%;
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                                                                    Query Match 88.7
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.5
Matches 10; Conservative
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                                                                                                                                                                                                      112 NFKLKHYGAGW 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 NFKLKHYGAGW 137
AA;
                                                                                                                                                                         1 NFKLKHYGPGW 11
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205
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SEQUENCE
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RESULT Q27774 ID Q2 AC Q2 DT Q1 DT Q1 DT Q1 DT Q1 DE PE DE DE B) OS SS

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Gaps

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Length 213; Indels S

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EU Arabidopsis sequencing project;
                                                                              Schistosoma.
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                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brasslcales; Brasslcaceae; Arabidopsis.
                         Gaps
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. WASSILEWSKIJA;
STRAIN-CV. WASSILEWSKIJA;
Mutations in a new Arabidopsis cyclophilin disrupt interaction with protein phosphatase 2A.";
Mol. Gen. Genet. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                COLORS: 7.31-63(2000).

1- FUNCTION: PEPTIDIAL OIS JOUGHT OF DAR RES. 7.31-63(2000).

1- FUNCTION: PEPTIDIAL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).

1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.

EMBL; AF123490; AAF05760.1; -
EMBL; AB020755; BAA97339.1; -
INTERIPO: IRRO02130; CSA_PPIASE.
                                                                                                                                                                                                                                                                                                                                     STRAIN-COLUMBIA;
MEDLINE-20181125; PubMed-10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 204;
   DB 6; Length 87;
0.043;
                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 AA; 21961 MW; CE2967AB4F65AF44 CRC64;
                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLOPHILIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.2%; Score 52; DB 10;
81.8%; Pred. No. 0.23;
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1; Mismatches
                                                                                                                  204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 AA
76.1%; Score 54; DB 100.0%; Pred. No. 0.0
                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00160; pro isomerase; 1. PRINTS; PR00153; CSAPPISMRASE. PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 09, (TrEMBLrel. 09,
                    B; Conservative
                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 73.2
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 NFKLKHTGPGF 135
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Ouery Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
                                         4 LKHYGPGW 11
                                                    1 LKHYGPGW 8
                                                                                                                                                                                                                                NCBI_TaxID=3702;
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Q26551;
01-JAN-1999 (
01-JAN-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isomerase;
SEQUENCE
                                                                                                                           Q9SP02;
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09SP02
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CYCLOPILIN and its expression in Escherichia coli.";

Mol. Biochem. Parasitol. 75:99-111(1995).

-! FUNCTION: PPLASES ACCELERATE THE FOLDING OF PROTEINS.

-! CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

-! ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.

-! SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).

-! BEVELOPMENTAL STAGE: THIS SOLUBLE PROTEIN IS PRESENT IN ABUNDANCE IN THE ADULT WORM AS WELL AS IN THE SCHISTOSOMULA AND THE EGGS.

-! SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPLASE PAMILY.
                                                                                                          Schistosoma mansoni (Blood fluke).
Eukaryota; Metazou; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
(ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYCLOPHILIN-LIKE PROTEIN.
R27K19_100.
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of a Schistosoma mansoni cDNA encoding a B-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PREVENT SECRETION FROM ER (BY SIMILARITY) SIMILARITY, CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rudd
                                                                                                                                                                                                                                                                                                                                                         Klinkert M.-Q., Bugli F., Engels B., Carrasquillo E., Valle C.,
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
STRAIN-PUERTO RICAN;
MEDLINE-96362065; Pubwed-8720179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 AA; 23294 MW;
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72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 72./*,
Loc 8; Conservative
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120 NFKLRHVGAGW 130
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                                                                                                                                                                                                                     NCBI_TaxID=6183;
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NCBI_TaxID=3702;
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01-NOV-1996
01-NOV-1996
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             038901;
038867;
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Q38901
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--- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
FRANS ISOMERASE FAMILY.
HANS 198797; AABOLS31.1; --
HSSP; P05092; 2CPL.
SEQUENCE FROM N.A.
MEDLINE-96165729; Pubmed-8587897;
Korneev S., Blackshaw S.E., Kaiser K., Davies J.A.;
"CDNA libraries from identified neurons.";
Proc. R. Soc. Lond., B. Blol. Sci. 263:57-62(1996).
-1- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOLDING OF PROTEINS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                 Score 52; DB 10; Length 234;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.8%; Score 51; DB 5; Length 143; 90.0%; Pred. No. 0.24; 1; Indels 1ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 AA; 15398 MW; 64FFD82018480A6B CRC64;
                                                                                                                                                                                                                                                                                                     234 AA; 25105 MW; 5CB22BBB363C2450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CYCLOPHILIN-A (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 AA
                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INSEF; FUG. 19R002130; CSA_PPIBASE.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                EMBL, ALI63832; CAB87846.1; ...
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 2.
PRIMTS; PR00153; CSA_PPISMSE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                   73.2%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01,
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                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 NFKLKHTGPGF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NFKLKHYGPGW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NFKLKHYGPG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFKLKHTGPG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-6421;
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                                                                                                                                                                                                                                                                                   (somerase;
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Q25093;
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Q25093
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RESULT 14 Q38867

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STRAIN=LANDSBERG:
A Saito T., Ashida H., Kawamukai M., Matsuda H., Nakagawa T.;
STRAIN=LANDSBERG:
L. Submitted (JUL-1995) to the EMBL/Genbank/DDBJ databases.
L. Submitted (JUL-1995) to the EMBL/Genbank/DDBJ databases.
- I- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
C - CATALTIC CATIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
- I- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
TRANS ISOMERASE FAMILY.
C PEMBL: U31370; AAA74096.1; -.
R HSSP; POS092; ICWL.
R HSSP; POS092; ICWL.
R HSSP; POS092; ICWL.
R HSSP; POS093; ICWL.
R HSSP; POS093; ICWL.
R HSSP; POS096; ICWL.
R PRINTS; PROUSES: ISOMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta; eudicotyledons: core eudicots: Rosidae:
eurosids II: Brassicales: Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CISTRANS ISOMERASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18969 MW; 24C2031B6CA107A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                        (TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 AA
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Pred. No.
                                         (TrEMBLrel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOSOLIC CYCLOPHILIN (EC 5.2.1.8).
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-COLUMBIA; MEDLINE-98088013; PubMed-9426607;
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 71.8
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                    CYCLOPHILIN (EC 5.2.1.8).
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PRELIMINARY;
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SEQUENCE '176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NFKLKHYGPG 10
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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DR HSSP; P05092; 1CWL.

DR Mendel; 6283; Arath;1040;6283.

DR InterPro; IPR00130; CSA_PPIase.

DR PRINTS; PR00163; CSA_PPIASE.

DR PROSITE; P500170; CSA_PPIASE.

DR PROSITE; P550072; CSA_PPIASE.1: 1.

DR PROSITE; P550072; CSA_PPIASE.2: 1.

KW ISOMERASE.

SQUENCE 176 AA; 18906 MW; 24C2031B6BC4DD90 CRC64;

QUETY MATCH

Best Local Similarity 90.0%; Pred. No. 0.3;

Matches 9; Conservative 0; Mismatches 1; Indels

OY INFKLKHYGPG 10

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Db 94 NFKLKHTGPG 103
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Search completed: January 15, 2002, 13:16:26 Job time: 657 sec

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0; Gaps

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